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=> s ((gene#(10a)(disrupt? or interrupt?))(30a)(marker? or reporter?))/bi,ab 1666570 GENE#/BI 1285415 GENE#/AB 155191 DISRUPT?/BI 143426 DISRUPT?/AB 51889 INTERRUPT?/BI 50007 INTERRUPT?/AB 361937 MARKER?/BI 304601 MARKER?/AB 71167 REPORTER?/BI 63325 REPORTER?/AB
L1 670 ((GENE#(10A)(DISRUPT? OR INTERRUPT?))(30A)(MARKER? OR REPORTER?))/BI,AB

=> s (yeast or saccharomyces or cerevisiae)/bi,ab 253530 YEAST/BI 207838 YEAST/AB 111428 SACCHAROMYCES/BI 64257 SACCHAROMYCES/AB 103822 CEREVISIAE/BI 69382 CEREVISIAE/AB
L2 291491 (YEAST OR SACCHAROMYCES OR CEREVISIAE)/BI,AB

=> s l1 and l2
L3 178 L1 AND L2

=> s l3 not 2011/py 600819 2011/PY
L4 172 L3 NOT 2011/PY

=> s l4 not 2010/py 1933915 2010/PY
L5 167 L4 NOT 2010/PY

=> s l5 not 2009/py 1912317 2009/PY
L6 159 L5 NOT 2009/PY

=> s l6 not 2008/py 1810285 2008/PY
L7 150 L6 NOT 2008/PY

=> s l7 not 2007/py 1729373 2007/PY
L8 140 L7 NOT 2007/PY

=> s l8 not 2006/py 1591787 2006/PY
L9 131 L8 NOT 2006/PY

=> s l9 not 2005/py 1437102 2005/PY
L10 116 L9 NOT 2005/PY

=> s l10 not 2004/py 1355248 2004/PY
L11 112 L10 NOT 2004/PY

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FILE 'CAPLUS' ENTERED AT 16:02:19 ON 28 APR 2011
L1 670 S ((GENE#(10A)(DISRUPT? OR INTERRUPT?))(30A)(MARKER? OR REPORTE
L2 291491 S (YEAST OR SACCHAROMYCES OR CEREVISIAE)/BI,AB
L3 178 S L1 AND L2
L4 172 S L3 NOT 2011/PY
L5 167 S L4 NOT 2010/PY
L6 159 S L5 NOT 2009/PY
L7 150 S L6 NOT 2008/PY
L8 140 S L7 NOT 2007/PY
L9 131 S L8 NOT 2006/PY
L10 116 S L9 NOT 2005/PY
L11 112 S L10 NOT 2004/PY

=> d l11 1-112 bib ab

L11 ANSWER 1 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2004:961215 CAPLUS <<LOGINID::20110428>>
DN 142:149766
TI Yarrowia lipolytica TRP1 gene, and expression vector and multiple gene disruption system using the same
IN Jun, Seon A.; Kang, Hyeon A.; Kim, Jeong Yun
PA Leadbio, Inc., S. Korea
SO Repub. Korean Kongkae Taeho Kongbo, No pp. given
CODEN: KRXXA7
DT Patent
LA Korean
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI KR 2003037490 A 20030514 KR 2001-68677 20011105
PRAI KR 2001-68677 20011105
AB A TRP1 gene of the ***yeast*** , Yarrowia lipolytica, and its use as a selection ***marker*** gene are provided to widen the range of selection ***genes*** available in Y. lipolytica and to manuf. a multiple ***gene*** ***disruption*** system using 5-fluoroanthranilic acid (5-FAA). A TRP1 gene of the ***yeast*** , Y. lipolytica was deposited in the Korean Collection for Type Cultures with the accession no. KCTC 0998BP, and a vector system was constructed by using the TRP1 gene as a selection marker gene. A multiple gene disruption system was manufd. by using the fact that Yarrowia lipolytica with the TRP1 gene has no viability in a medium contg. 5-FAA, however, Yarrowia lipolytica with a disrupted TRP1 gene was viable therein.

L11 ANSWER 2 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2004:948196 CAPLUS <<LOGINID::20110428>>
DN 142:128689
TI Method for selecting putative endocrine disrupting chemicals (EDCs) using ***yeast*** two-hybrid system and transformed ***yeast*** used in the same method
IN Lee, Hyeon Ju; Lee, Kee Sook; Lee, Yong Su
PA S. Korea
SO Repub. Korean Kongkae Taeho Kongbo, No pp. given
CODEN: KRXXA7
DT Patent
LA Korean
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI KR 2003025132 A 20030328 KR 2001-58086 20010919
PRAI KR 2001-58086 20010919
AB A method for selecting putative endocrine disrupting chems.(EDCs) using ***yeast*** two-hybrid system and transformed ***yeast*** used in the same method are provided, which method has similar sensitivity to the prior method using mammal cells, and the endocrine disrupting chems.(EDCs) can be easily selected by the method. The method for selecting putative endocrine disrupting chems.(EDCs) using ***yeast*** two-hybrid system comprises the steps of: culturing transformed ***yeast*** having a first expression vector contg. a first protein gene fused by a DNA-binding domain and a sex hormone receptor or a ligand-binding domain of the sex hormone receptor, a second expression vector expressing a second protein gene fused by a coactivator of the sex hormone receptor and a transcription activating domain, and a third expression vector expressing a ***reporter*** gene operably linked to a recognition site of the DNA-binding domain together with putative endocrine ***disrupting*** chem.; and analyzing the transcription activity of the ***reporter***

gene to det. whether the putative endocrine ***disrupting*** chem. is antagonist or agonist of the ***reporter*** ***gene*** , wherein the sex hormone receptor gene is androgen receptor gene; the ***reporter*** gene is selected from -galactosidase, HIS3, Leu2 or URA3; the first vector is pLexA-ARhLBD; the second vector is pB42-ASC1; and the third vector is p8op-lacZ.

L11 ANSWER 3 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2004:10572 CAPLUS <<LOGINID::20110428>>
DN 140:194224
TI Cloning and sequence analysis of the TRP1 gene encoding the phosphoribosyl anthranilate isomerase from Pichia anomala (strain K)
AU Friel, Damien; Vandenbol, Micheline; Jijakli, M. Haissam
CS Plant Pathology Unit, University of Agricultural Sciences, Gembloux, 5030, Belg.
SO Yeast (2003), 20(16), 1331-1337 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Pichia anomala (strain K) is an efficient biocontrol agent against post-harvest diseases affecting apples. To study the role of strain K genes in biocontrol activity, it is useful to identify selectable ***markers*** on which to base a ***gene*** ***disruption*** strategy. The Pichia anomala TRP1 gene (PaTRP1) was isolated by complementation of the multi-auxotrophic S. ***cerevisiae*** strain FY-1679-18b. DNA sequence anal. revealed the presence of a 699 bp ORF encoding a 233 amino acid protein showing the typical conserved structure of proteins of the phosphoribosyl anthranilate isomerase (PRAI) family. Codon anal. revealed a high no. of unused codons. Downstream from PaTRP1 was found the 3' extremity of a gene highly similar to the IPP1 gene (coding for the inorg. pyrophosphatase). In addn., a sequence of the 5' extremity of the insert is highly similar to a fragment of the S. ***cerevisiae*** PRP9 gene, coding for a spliceosome-assocd. protein. The nucleotide sequence has been deposited in the Genbank database under Accession No. AY198188.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 4 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:938250 CAPLUS <<LOGINID::20110428>>
DN 140:269864
TI Application of the reuseable, KanMX selectable marker to industrial ***yeast*** : construction and evaluation of heterothallic wine strains of ***Saccharomyces*** ***cerevisiae*** , possessing minimal foreign DNA sequences
AU Walker, Michelle E.; Gardner, Jennie M.; Vystavelova, Andrea; McBryde, Colin; de Barros Lopes, Miguel; Jiranek, Vladimir
CS School of Agriculture and Wine, The University of Adelaide, Glen Osmond, 5064, Australia
SO FEMS Yeast Research (2003), 4(3), 339-347 CODEN: FYREAG; ISSN: 1567-1356
PB Elsevier Science B.V.
DT Journal
LA English
AB The authors identified com. wine strains with good mating and sporulation properties from which heterothallic derivs. were constructed by disruption of the HO gene. Consequently, these haploids are amenable to genetic anal., while retaining desirable wine-making properties. The approach used was an adaptation of a previously published ***gene*** ***disruption*** procedure for lab. ***yeast*** and is based on the acquisition of geneticin resistance from a removable KanMX ***marker*** . The present work is the first report of the application of a construct of this type to the disruption of the HO gene in wine yeasts that are in common com. use. Most of the 4.9-kb disruption construct was successfully removed from the genome of the haploid deriv. strains by loop-out of the KanMX marker through meiotic recombination. Sequencing of the HO region confirmed the redn. of foreign sequences to a 582-bp fragment comprised largely of a single direct repeat at the target gene. The removal of the active foreign gene (conferring antibiotic resistance) allows the application of other constructs based on the KanMX module without the need to resort to other selectable marker systems. Lab.-scale fermn. trials typically showed minimal differences between the HO disruptants and the parental wine strains in terms of fermn. kinetics and formation of key metabolites.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 5 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:881207 CAPLUS <<LOGINID::20110428>>
DN 140:123564
TI Regulation of the Hansenula polymorpha maltase gene promoter in H. polymorpha and ***Saccharomyces*** ***cerevisiae***
AU Alamae, Tiina; Parn, Pille; Viigand, Katrin; Karp, Helen
CS Institute of Molecular and Cell Biology, University of Tartu, Tartu, 51010, Estonia
SO FEMS Yeast Research (2003), 4(2), 165-173 CODEN: FYREAG; ISSN: 1567-1356
PB Elsevier Science B.V.
DT Journal
LA English
AB Hansenula polymorpha is an exception among methylotrophic yeasts because it can grow on the disaccharides maltose and sucrose. The authors disrupted the maltase gene (HPMAL1) in H. polymorpha 201 using homologous recombination. Resulting disruptants HP201HPMAL1.DELTA. failed to grow on maltose and sucrose, showing that maltase is essential for the growth of H. polymorpha on both disaccharides. Expression of HPMAL1 in HP201HPMAL1.DELTA. from the truncated variants of the promoter enabled the authors' to define the 5'-upstream region as sufficient for the induction of maltase by disaccharides and its repression by glucose. Expression of the ***Saccharomyces*** ***cerevisiae*** maltase gene MAL62 was induced by maltose and sucrose, and repressed by glucose if expressed in HP201HPMAL1.DELTA. from its own promoter. Similarly, the HPMAL1 promoter was recognized and correctly regulated by the carbon source in a S. ***cerevisiae*** maltase-neg. mutant 100-1B. Therefore the authors suggest that the transcriptional regulators of S. ***cerevisiae*** MAL genes (MAL activator and Mig1 repressor) can affect the expression of the H. polymorpha maltase gene, and that homologs of these proteins may exist in H. polymorpha. Using the HPMAL1 ***gene*** as a ***reporter*** in a H. polymorpha maltase ***disruption*** mutant it was shown that the strength of the HPMAL1 promoter if induced by sucrose is quite comparable to the strength of the H. polymorpha alc. oxidase promoter under conditions of methanol

induction, revealing the biotechnol. potential of the HPMAL1 promoter.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 6 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:866533 CAPLUS <<LOGINID::20110428>>
DN 140:265059
TI New ***disruption*** cassettes for rapid ***gene*** ***disruption*** and ***marker*** rescue in the ***yeast*** Yarrowia lipolytica
AU Fickers, P.; Le Dall, M. T.; Gaillardin, C.; Thonart, P.; Nicaud, J. M.
CS CNRS INRA INAP-G UMR2585, Laboratoire Microbiologie et Genetique Moleculaire, Institut National Agronomique Paris-Grignon, Thiverval-Grignon, F-78850, Fr.
SO Journal of Microbiological Methods (2003), 55(3), 727-737 CODEN: JMIMDQ; ISSN: 0167-7012
PB Elsevier Science B.V.
DT Journal
LA English
AB Yarrowia lipolytica is one of the most extensively studied nonconventional yeasts. Unfortunately, few methods for gene disruption have been reported for this ***yeast*** , and all of them are time-consuming and laborious. The functional anal. of unknown genes requires powerful disruption methods. Here, we describe such a new method for rapid gene disruption in Y. lipolytica. This knockout system combines SEP method and the Cre-lox recombination system, facilitating efficient marker rescue. Versatility was increased by using both auxotrophic markers like yIURA3 and yILEU2, as well as the antibiotic resistance marker hph. The hph ***marker*** , which confers resistance to hygromycin-B, allows ***gene*** ***disruption*** in a strain lacking any conventional auxotrophic ***marker*** . The disruption cassette was shown to integrate at the correct locus at an av. frequency of 45%. Upon expression of Cre recombinase, the marker was excised at a frequency of 98%, by recombination between the two lox sites. This new method for gene disruption is an ideal tool for the functional anal. of gene families, or for creating large-scale mutant collections in general.
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 7 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:660984 CAPLUS <<LOGINID::20110428>>
DN 139:302695
TI New " ***marker*** swap" plasmids for converting selectable ***markers*** on budding ***yeast*** ***gene*** ***disruptions*** and plasmids
AU Voth, Warren P.; Jiang, Yi Wei; Stillman, David J.
CS Department of Pathology University of Utah, Salt Lake City, UT, 84132, USA
SO Yeast (2003), 20(11), 985-993 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB ***Marker*** swap plasmids can be used to change ***markers*** for ***genes*** ***disrupted*** with nutritional ***markers*** in the ***yeast*** ***Saccharomyces*** ***cerevisiae*** . We describe 18 new marker swap plasmids, and we also review other plasmids available for marker conversions. All of these plasmids have long regions of flanking sequence identity, and thus the efficiency of homologous recombination mediated by marker conversion is very high. Marker swaps allow one to easily perform crosses to construct double mutant strains even if each of the disrupted strains contains the same marker, as is the case with the KanMX marker used in the ***yeast*** knockout collection. Marker swaps can also be used to change the selectable marker on plasmids, eliminating the need for subcloning.
OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 8 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:500229 CAPLUS <<LOGINID::20110428>>
DN 139:160618
TI Isolation and characterization of the TRP1 gene from the ***yeast*** Yarrowia lipolytica and multiple gene disruption using a TRP blaster
AU Cheon, Seon Ah; Han, Eun Jung; Kang, Hyun Ah; Ogrydziak, David M.; Kim, Jeong-Yoon
CS Department of Microbiology, Chungnam National University, Daejeon, 305-764, S. Korea
SO Yeast (2003), 20(8), 677-685 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB The TRP1 gene encoding N-(5'-phosphoribosyl)-anthranilate isomerase was isolated from the ***yeast*** Yarrowia lipolytica, in which only a few genetic marker genes are available. The Y. lipolytica TRP1 gene (YITRP1) cloned by complementation of Y. lipolytica trp1 mutation was found to be a functional homolog of ***Saccharomyces*** ***cerevisiae*** TRP1. Since YITRP1 could be used for counterselection in medium contg. 5-fluoroanthranilic acid (5-FAA), we constructed TRP blasters that contained YITRP1 flanked by a direct repeat of a sequence and allowed the recycling of the YITRP1 marker. Using the TRP blasters the sequential disruption of target genes could be carried out within the same strain of Y. lipolytica. The nucleotide sequence of the YITRP1 gene has been deposited at GenBank under Accession No. AF420590.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 9 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:202122 CAPLUS <<LOGINID::20110428>>
DN 138:363358
TI Ends-out, or replacement, gene targeting in Drosophila
AU Gong, Wei J.; Golic, Kent G.
CS Stowers Institute for Medical Research, Kansas City, MO, 64110, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2003), 100(5), 2556-2561 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English

AB Ends-in and ends-out refer to the two arrangements of donor DNA that can be used for gene targeting. Both have been used for targeted mutagenesis, but require donors of differing design. Ends-out targeting is more frequently used in mice and ***yeast*** because it gives a straightforward route to replace or delete a target locus. Although ends-in targeting has been successful in Drosophila, an attempt at ends-out targeting failed. To test whether ends-out targeting could be used in Drosophila, we applied two strategies for ends-out gene replacement at the endogenous yellow (y) locus in Drosophila. First, a mutant allele was rescued by replacement with an 8-kb y+ DNA fragment at a rate of .apprxeq.1/800 gametes. Second, a wild-type ***gene*** was ***disrupted*** by the insertion of a ***marker*** ***gene*** in exon 1 at a rate of .apprxeq.1/380 gametes. The I-SceI endonuclease component alone is not sufficient for targeting: the FLP recombinase is also needed to generate the extrachromosomal donor. When both components are used we find that ends-out targeting can be approx. as efficient as ends-in targeting, and is likely to be generally useful for Drosophila gene targeting.
OSC.G 118 THERE ARE 118 CAPLUS RECORDS THAT CITE THIS RECORD (118 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 10 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:97548 CAPLUS <<LOGINID::20110428>>
DN 138:148653
TI Methods for in-frame gene disruption by homologous recombination and uses for gene discovery
IN Awrey, Donald E.; Greenblatt, Jack
PA Affinium Pharmaceuticals, Inc. Agency for Defence Development, Can.
SO PCT Int. Appl., 56 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2003010333 A2 20030206 WO 2002-CA1160 20020724 WO 2003010333 A3 20031030 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2002355155 A1 20030217 AU 2002-355155 20020724 US 20030082591 A1 20030501 US 2002-202442 20020724
PRAI US 2001-307461P P 20010724 WO 2002-CA1160 W 20020724
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The present invention relates to compns. and methods for in-frame disruption of a gene sequence by homologous recombination. Specifically, the invention uses a targeting polynucleotide comprising a mol. tag, which maybe a random sequence that does not occur in the host cell or a sequence encoding for a protein capable of generating a selectable or detectable signal, and flanking homol. clamps for in-frame disruption of a target gene. The present invention may be used in certain embodiments to disrupt a gene without causing any downstream effects on non-target sequences. In certain embodiments, the inventive methods may be used to identify and/or characterize products encoded by essential genes, conditionally essential genes, and non-essential genes.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 11 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:980286 CAPLUS <<LOGINID::20110428>>
DN 138:315980
TI Development of a simple screening system for endocrine disruptors
AU Sugawara, Teruo; Nakajima, Ayako; Nomura, Eiji
CS Department of Biochemistry, Hokkaido University School of Medicine, Sapporo, Hokkaido, Japan
SO Medical Science Monitor (2002), 8(11), BR431-BR438 CODEN: MSMOFR; ISSN: 1234-1010
PB International Scientific Literature, Inc.
DT Journal
LA English
AB Background: An endocrine disruptor is a synthetic chem., which causes adverse effects in an organism, or its progeny, after causing perturbations in the endocrine system. It is important to know which synthetic chems. have endocrine-disrupting action. However, an increasing no. of synthetic chems. are being produced by modern synthetic chem., and the examn. of endocrine disruptor potential has not yet caught up with the advances in synthetic chem. In this study, we have developed such a screening system for detecting synthetic chems. with estrogen-like effects. Material/Methods: The system was based on the ***yeast*** one-hybrid system. Both HIS3 and lacZ reporter genes connected to three tandem copies of the estrogen response element were prepd. Gal4-estrogen receptor is a fusion protein made from the activation domain (AD) of the ***yeast*** GAL4 transactivator gene and then incorporated into a plasmid, which was transfected into the YM4271 ***yeast*** cell strain. The estrogen effect was judged by this developed screening system. Results: A dual reporter assay-system was established by transfection of the both HIS3 and lacZ reporter genes into the ***yeast*** cells. This screening system enabled the detection of as little as 10-12 mol of .beta.-estradiol. Conclusion: These results show that this newly developed dual assay is useful for the screening of endocrine-disruptors that have estrogen-like action.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 12 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:966196 CAPLUS <<LOGINID::20110428>>
DN 138:232271
TI Molecular cell biology and molecular genetics of Histoplasma capsulatum
AU Ignatov, Atanas; Keath, Elizabeth J.
CS Department of Biology, Saint Louis University, St. Louis, MO, 63103, USA

SO International Journal of Medical Microbiology (2002), 292(5-6), 349-361 CODEN: IMEMFV; ISSN: 1438-4221
PB Urban & Fischer Verlag GmbH & Co. KG
DT Journal; General Review
LA English
AB A review. Histoplasma capsulatum is a dimorphic ascomycete which is capable of producing a broad spectrum of disease ranging from mild asymptomatic, pulmonary illness to severe, life-threatening systemic mycosis. Regulatory mechanisms that use temp. and other environmental cues are paramount to the successful adaptation of the organism as an effective intracellular pathogenic ***yeast*** . Although the biochem. and phenomenol. of reversible morphogenesis have been well examd. in Histoplasma, the identification and functional characterization of genes and their products that are required for early establishment or maintenance of the parasitic ***yeast*** phase in intracellular host compartments have only recently been fruitful. Advances in the mol. biol. of Histoplasma, including approaches to introduce telomeric plasmids, ***reporter*** fusion constructs, and ***gene*** ***disruption*** cassettes into the fungus are poised to solidify the pre-eminence of this fungus as a model system which can be applied to other dimorphic fungal pathogens that exhibit similar cellular and immunol. complexities. This review centers on recent developments in the mol. cell biol. and mol. genetics of Histoplasma capsulatum that provide important new avenues for examg. the mold-to- ***yeast*** phase transition beyond the historical, binary view of dimorphism and the implications that these successful approaches may have on seminal issues in fungal pathogenesis.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)
RE.CNT 95 THERE ARE 95 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 13 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:937303 CAPLUS <<LOGINID::20110428>>
DN 138:20443
TI Endocrine disruptor screening using DNA chips of endocrine disruptor-responsive genes
IN Kondo, Akihiro; Takeda, Takeshi; Mizutani, Shigetoshi; Tsujimoto, Yoshimasa; Takashima, Ryokichi; Enoki, Yuki; Kato, Ikunoshin
PA Takara Bio Inc., Japan
SO Jpn. Kokai Tokkyo Koho, 386 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI JP 2002355079 A 20021210 JP 2002-69354 20020313
PRAI JP 2001-73183 A 20010314 JP 2001-74993 A 20010315 JP 2001-102519 A 20010330
AB A method and kit for detecting endocrine-disrupting chems. using DNA microarrays are claimed. The method comprises prepg. a nucleic acid sample contg. mRNAs or cDNAs originating in cells, tissues, or organisms which have been brought into contact with a sample contg. the endocrine disruptor. The nucleic acid sample is hybridized with DNA microarrays having genes affected by the endocrine disruptor or DNA fragments originating in these genes have been fixed. The results obtained are then compared with the results obtained with the control sample to select the gene affected by the endocrine disruptor. Genes whose expression is altered by tri-Bu tin, 4-octaphenol, 4-nonylphenol, di-N-Bu phthalate, dichlorohexyl phthalate, octachlorostyrene, benzophenone, diethylhexyl phthalate, diethylstilbestrol (DES), and 17-.beta. estradiol (E2), were found in mice by DNA chip anal.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L11 ANSWER 14 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:846053 CAPLUS <<LOGINID::20110428>>
DN 138:131920
TI Cloning and characterization of the nagA gene that encodes .beta.-N-acetylglucosaminidase from Aspergillus nidulans and its expression in Aspergillus oryzae
AU Kim, Sunhwa; Matsuo, Ichiro; Ajisaka, Katsumi; Nakajima, Harushi; Kitamoto, Katsuhiko
CS Department of Biotechnology, University of Tokyo, Tokyo, 113-8657, Japan
SO Bioscience, Biotechnology, and Biochemistry (2002), 66(10), 2168-2175 CODEN: BBBIEJ; ISSN: 0916-8451
PB Japan Society for Bioscience, Biotechnology, and Agrochemistry
DT Journal
LA English
AB We isolated a .beta.-N-acetylglucosaminidase encoding gene and its cDNA from the filamentous fungus Aspergillus nidulans, and designated it nagA. The nagA gene contained no intron and encoded a polypeptide of 603 amino acids with a putative 19-amino acid signal sequence. The deduced amino acid sequence was very similar to the sequence of Candida albicans Hex1 and Trichoderma harzianum Nag1. ***Yeast*** cells contg. the nagA cDNA under the control of the GAL1 promoter expressed .beta.-N-acetylglucosaminidase activity. The chromosomal nagA ***gene*** of A. nidulans was ***disrupted*** by replacement with the argB ***marker*** ***gene*** . The disruptant strains expressed low levels of .beta.-N-acetylglucosaminidase activity and showed poor growth on a medium contg. chitobiose as a carbon source. Aspergillus oryzae strain carrying the nagA gene under the control of the improved glaA promoter produced large amts. of .beta.-N-acetylglucosaminidase in a wheat bran solid culture.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 15 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:806897 CAPLUS <<LOGINID::20110428>>
DN 138:298379
TI Generation of disruption cassettes in vivo using a PCR product and ***Saccharomyces*** ***cerevisiae***
AU Zaragoza, Oscar
CS Instituto de Investigaciones Biomedicas "Alberto Sols" CSIC-UAM, Madrid, 28029, Spain
SO Journal of Microbiological Methods (2003), 52(1), 141-145 CODEN: JMIMDQ; ISSN: 0167-7012
PB Elsevier Science B.V.
DT Journal
LA English
AB A method to obtain disruption cassettes based on the homologous recombination in ***Saccharomyces*** ***cerevisiae*** is described. The disruption ***marker*** is amplified by PCR using oligonucleotides contg. 50 bp

homologous to the ***disruptable*** ***gene*** and 20 bp from the ***marker*** . The PCR product is cotransformed into ***yeast*** with a plasmid contg. the gene. After recombination, a plasmid that carries the disruption cassette for the gene is produced.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 16 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:743062 CAPLUS <<LOGINID::20110428>>
DN 138:69604
TI A novel membrane protein, Ros3p, is required for phospholipid translocation across the plasma membrane in ***Saccharomyces*** ***cerevisiae***
AU Kato, Utako; Emoto, Kazuo; Fredriksson, Charlotta; Nakamura, Hidemitsu; Ohta, Akinori; Kobayashi, Toshihide; Murakami-Murofushi, Kimiko; Kobayashi, Tetsuyuki; Umeda, Masato
CS Department of Molecular Biodynamics, Tokyo Metropolitan Institute of Medical Science, Tokyo, 113-8613, Japan
SO Journal of Biological Chemistry (2002), 277(40), 37855-37862 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Ro09-0198 (Ro) is a tetracyclic peptide antibiotic that binds specifically to phosphatidylethanolamine (PE) and causes cytolysis. To investigate the mol. basis of transbilayer movement of PE in biol. membranes, we have isolated a series of budding ***yeast*** mutants that are hypersensitive to the Ro peptide. One of the most sensitive mutants, designated ros3 (Ro-sensitive 3), showed no significant change in the cellular phospholipid compn. or in the sensitivity to amphotericin B, a sterol-binding polyene macrolide antibiotic. These results suggest that the mutation of ros3 affects the PE organization on the plasma membrane, rather than PE synthesis or overall organization of the membrane structures. By functional complementation screening, we identified the gene ROS3 affected in the mutant, and we showed that the hypersensitive phenotype was caused by the defective expression of the ROS3 gene product, Ros3p, an evolutionarily conserved protein with two putative transmembrane domains. ***Disruption*** of the ROS3 ***gene*** resulted in a marked decrease in the internalization of fluorescence-labeled analogs of PE and phosphatidylcholine, whereas the uptake of fluorescence-labeled phosphatidylserine and endocytic ***markers*** was not affected. Neither expression levels nor activities of ATP-binding cassette transporters of the ros3.DELTA. cells differed from those of wild type cells, suggesting that Ros3p is not related to the multidrug resistance activities. Immunochem. analyses of the structure and subcellular localization showed that Ros3p was a glycosylated membrane protein localized in both the plasma membrane and the endoplasmic reticulum, and that a part of Ros3p was assocd. with the detergent-insol. glycolipid-enriched complexes. These results indicate that Ros3p is a membrane glycoprotein that plays an important role in the phospholipid translocation across the plasma membrane.
OSC.G 56 THERE ARE 56 CAPLUS RECORDS THAT CITE THIS RECORD (56 CITINGS)
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 17 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:612739 CAPLUS <<LOGINID::20110428>>
DN 137:321173
TI The fission ***yeast*** ubiquitin-conjugating enzymes Ubcp3, Ubc15, and Rhp6 affect transcriptional silencing of the mating-type region
AU Nielsen, Inga Sig; Nielsen, Olaf; Murray, Johanne M.; Thon, Genevieve
CS Department of Genetics, Institute of Molecular Biology, University of Copenhagen, Copenhagen K, DK-1353, Den.
SO Eukaryotic Cell (2002), 1(4), 613-625 CODEN: ECUEA2; ISSN: 1535-9778
PB American Society for Microbiology
DT Journal
LA English
AB Genes transcribed by RNA polymerase II are silenced when introduced near the mat2 or mat3 mating-type loci of the fission ***yeast*** Schizosaccharomyces pombe. Silencing is mediated by a no. of gene products and cis-acting elements. We report here the finding of novel trans-acting factors identified in a screen for high-copy-no. disruptors of silencing. Expression of cDNAs encoding the putative E2 ubiquitin-conjugating enzymes UbcP3, Ubc15 (ubiquitin-conjugating enzyme), or Rhp6 (Rad homolog pombe) from the strong nmt1 promoter derepressed the silent mating-type loci mat2 and mat3 and reporter genes inserted nearby. Deletion of rhp6 slightly derepressed an ade6 ***reporter*** ***gene*** placed in the mating-type region, whereas ***disruption*** of ubcP3 or ubc15 had no obvious effect on silencing. Rhp18 is the S. pombe homolog of ***Saccharomyces*** ***cerevisiae*** Rad18p, a DNA-binding protein that phys. interacts with Rad6p. Rhp18 was not required for the derepression obsd. when UbcP3, Ubc15, or Rhp6 was overproduced. Overexpressing Rhp6 active-site mutants showed that the ubiquitin-conjugating activity of Rhp6 is essential for disruption of silencing. However, high dosage of UbcP3, Ubc15, or Rhp6 was not suppressed by a mutation in the 26S proteasome, suggesting that loss of silencing is not due to an increased degrdn. of silencing factors but rather to the posttranslational modification of proteins by ubiquitination. We discuss the implications of these results for the possible modes of action of UbcP3, Ubc15, and Rhp6.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 88 THERE ARE 88 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 18 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:283809 CAPLUS <<LOGINID::20110428>>
DN 137:17624
TI Sets of integrating plasmids and ***gene*** ***disruption*** cassettes containing improved counter-selection ***markers*** designed for repeated use in budding ***yeast***
AU Akada, Rinji; Hirosawa, Isao; Kawahata, Miho; Hoshida, Hisashi; Nishizawa, Yoshinori
CS Department of Applied Chemistry and Chemical Engineering, Faculty of Engineering, Yamaguchi University, Ube, 755-8611, Japan
SO Yeast (2002), 19(5), 393-402 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal

LA English
AB Counter-selection is a useful gene manipulation technique for repeated gene disruptions, gene shufflings and gene replacements in yeasts. We developed a novel counter-selection system using a galactose-inducible growth inhibitory sequence. This counter-selection marker, named GAL10p-GIN11, has several advantages over previous counter-selection markers, i.e. use of an inexpensive galactose medium for counter-selection, combined use with any transformation markers for gene introduction, and no requirement of specific mutations in the host strains. The GIN11 sequence, which is a part of an X-element of the subtelomeric regions, contained a conserved autonomously replicating sequence, causing the possibility of inefficient chromosomal integration. We isolated GIN11 mutants that lost the replication activity but retained the growth-inhibitory effect when overexpressed. A mutant GIN11M86 sequence was selected and fused to the CUP1 promoter for the counter-selection on a Cu-contg. medium. The GALp-GIN11M86 and the CUPp-GIN11M86 were used for constructing sets of integrating plasmids contg. auxotrophic markers involving HIS3, TRP1, LEU2, URA3 or ADE2, or a drug-resistant marker PGKp-YAP1. In addn., a set of ***gene*** ***disruption*** cassettes that contained each of the auxotrophic ***markers*** and the GALp-GIN11M86, which were flanked by direct repeats of a hisG sequence, were constructed. The counter-selectable integrating plasmids and the ***gene*** ***disruption*** cassettes can allow the ***markers*** to be used repeatedly for ***yeast*** gene manipulations.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 19 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:242754 CAPLUS <<LOGINID::20110428>>
DN 137:120281
TI A second set of loxP marker cassettes for Cre-mediated multiple gene knockouts in budding ***yeast***
AU Gueldener, U.; Heinisch, J.; Koehler, G. J.; Voss, D.; Hegemann, J. H.
CS Inst. Mikrobiologie, Heinrich-Heine-Univ., Duesseldorf, 40225, Germany
SO Nucleic Acids Research (2002), 30(6), e23/1-e23/8 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Heterologous markers are important tools required for the mol. dissection of gene function in many organisms, including ***Saccharomyces*** ***cerevisiae*** . Moreover, the presence of gene families and isoenzymes often makes it necessary to delete more than one gene. We recently introduced a new and efficient ***gene*** ***disruption*** cassette for repeated use in budding ***yeast*** , which combines the heterologous dominant kanr resistance ***marker*** with a Cre/loxP-mediated ***marker*** removal procedure. Here we describe an addnl. set of four completely heterologous loxP-flanked marker cassettes carrying the genes URA3 and LEU2 from Kluyveromyces lactis, his5+ from Schizosaccharomyces pombe and the dominant resistance marker bler from the bacterial transposon Tn5, which confers resistance to the antibiotic phleomycin. All five loxP- ***marker*** ***gene*** -loxP ***gene*** ***disruption*** cassettes can be generated using the same pair of oligonucleotides and all can be used for ***gene*** ***disruption*** with high efficiency. For marker rescue we have created three addnl. Cre expression vectors carrying HIS3, TRP1 or bler as the ***yeast*** selection marker. The set of disruption cassettes and Cre expression plasmids described here represents a significant further development of the marker rescue system, which is ideally suited to functional anal. of the S. ***cerevisiae*** genome.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 20 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:240046 CAPLUS <<LOGINID::20110428>>
DN 136:398267
TI Candida albicans sterol C-14 reductase, encoded by the ERG24 gene, as a potential antifungal target site
AU Jia, N.; Skaggs, B. Arthington; Lee, W.; Pierson, C. A.; Lees, N. D.; Eckstein, J.; Barbuch, R.; Bard, M.
CS Department of Biology, Indiana University Purdue University Indianapolis, Indianapolis, IN, 46202-5132, USA
SO Antimicrobial Agents and Chemotherapy (2002), 46(4), 947-957 CODEN: AMACCQ; ISSN: 0066-4804
PB American Society for Microbiology
DT Journal
LA English
AB The incidence of fungal infections has increased dramatically, which has necessitated addnl. and prolonged use of the available antifungal agents. Increased resistance to the commonly used antifungal agents, primarily the azoles, has been reported, thus necessitating the discovery and development of compds. that would be effective against the major human fungal pathogens. The sterol biosynthetic pathway has proved to be a fertile area for antifungal development, and steps which might provide good targets for novel antifungal development remain. The sterol C-14 reductase, encoded by the ERG24 gene, could be an effective target for drug development since the morpholine antifungals, inhibitors of Erg24p, have been successful in agricultural applications. The ERG24 gene of Candida albicans has been isolated by complementation of a ***Saccharomyces*** ***cerevisiae*** erg24 mutant. Both copies of the C. albicans ERG24 ***gene*** have been ***disrupted*** by using short homologous regions of the ERG24 ***gene*** flanking a selectable ***marker*** . Unlike S. ***cerevisiae*** , the C. albicans ERG24 gene was not required for growth, but erg24 mutants showed several altered phenotypes. They were demonstrated to be slowly growing, with doubling times at least twice that of the wild type. They were also shown to be significantly more sensitive to an allylamine antifungal and to selected cellular inhibitors including cycloheximide, cerulenin, fluphenazine, and brefeldin A. The erg24 mutants were also slightly resistant to the azoles. Most importantly, erg24 mutants were shown to be significantly less pathogenic in a mouse model system and failed to produce germ tubes upon incubation in human serum. On the basis of these characteristics, inhibitors of Erg24p would be effective against C. albicans.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 21 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN

AN 2002:214576 CAPLUS <<LOGINID::20110428>>
DN 137:89002
TI Efficient PCR-based gene disruption in ***Saccharomyces*** strains using intergenic primers
AU Reid, Robert J. D.; Sunjevaric, Ivana; Kedacche, Mehdi; Rothstein, Rodney
CS Department of Genetics and Development, Columbia University College of Physicians and Surgeons, New York, NY, 10032-2704, USA
SO Yeast (2002), 19(4), 319-328 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Gene disruptions are a vital tool for understanding ***Saccharomyces*** ***cerevisiae*** gene function. An arrayed library of gene disruption strains has been produced by a consortium of ***yeast*** labs.; however their use is limited to a single genetic background. Since the ***yeast*** research community works with several different strain backgrounds, disruption libraries in other common lab. strains are desirable. We have developed simple PCR-based methods that allow transfer of gene disruptions from the S288C-derived strain library into any ***Saccharomyces*** strain. One method transfers the unique sequence tags that flank each of the ***disrupted*** ***genes*** and replaces the kanamycin resistance ***marker*** with a recyclable URA3 gene from Kluyveromyces lactis. All gene-specific PCR amplifications for this method are performed using a pre-existing set of primers that are com. available. We have also extended this PCR technique to develop a second general gene disruption method suitable for any transformable strain of ***Saccharomyces*** .
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 22 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:79435 CAPLUS <<LOGINID::20110428>>
DN 137:17617
TI Disruption of six ***Saccharomyces*** ***cerevisiae*** ORFs on chromosome XII results in three lethal disruptants
AU Alloush, Habib M.; Edwards, Thomas A.; Valle-Lisboa, Virginia; Wheals, Alan E.
CS Department of Biology and Biochemistry, University of Bath, Bath, BA2 7AY, UK
SO Yeast (2002), 19(1), 79-86 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Six ORFs of unknown function from the left arm of chromosome XII of ***Saccharomyces*** ***cerevisiae*** were chosen for a reverse genetic approach to provide materials to assist in assignment of function. A two-step PCR using long-flanking homol. was employed to amplify ***disruption*** cassettes consisting of a kanMX ***gene*** as selectable ***marker*** flanked by 250-350 bp long regions homologous to the target gene. The diploid strains FY1679 and CEN.PK2 were transformed with the replacement cassettes and transformants were selected for geneticin (G418) resistance. Correct targeting of the replacement cassettes at the genomic locus was verified by Southern blot anal. with the kanMX gene as a probe. Disruption cassettes were cloned in pUG7 plasmid for systematic gene inactivation in other ***yeast*** strains and the cognate genes were cloned in pRS416 plasmid for gene complementation studies. Sporulation and tetrad anal. of heterozygous disruptants showed that three of the six ORFs [YLR141w (RRN5), YLR145w and YLR147c (SMD3)] were essential genes that were complemented by their cognate genes. Ylr146c.DELTA. (spe4) homozygous diploids showed enhanced sporulation efficiency, whereas ylr147c.DELTA. heterozygous diploids failed to sporulate in the FY1679 but not in the CEN.PK2 genetic background. The other two disruptants [ylr143w and ylr144c (acf2)] gave no phenotype.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 23 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:79429 CAPLUS <<LOGINID::20110428>>
DN 136:259809
TI Use of a YAP1 overexpression cassette conferring specific resistance to cerulenin and cycloheximide as an efficient selectable marker in the ***yeast*** ***Saccharomyces*** ***cerevisiae***
AU Akada, Rinji; Shimizu, Yoshirou; Matsushita, Yuji; Kawahata, Miho; Hoshida, Hisashi; Nishizawa, Yoshinori
CS Department of Applied Chemistry and Chemical Engineering, Faculty of Engineering, Yamaguchi University, Ube, 755-8611, Japan
SO Yeast (2002), 19(1), 17-28 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Drug-resistance markers for ***yeast*** transformation are useful because they can be applied to strains without auxotrophic mutations. However, they are susceptible to tech. difficulties, namely lower transformation efficiency and the appearance of drug-resistant mutants without the marker. To avoid these problems, we have constructed a phosphoglycerate kinase (PGK) promoter-driven YAP1 expression cassette, called PGKp-YAP1. ***Yeast*** cells contg. PGKp-YAP1 were resistant to cycloheximide, a protein synthesis inhibitor, and also to cerulenin, a fatty acid synthesis inhibitor, but not to other drugs tested. The transformation efficiency of PGKp-YAP1 using cerulenin selection was comparable to that using a URA3 auxotrophic marker when low concns. of cerulenin were used. Non-transformed drug-resistant colonies did appear on the low-concn. cerulenin plates. However, these non-transformed colonies could easily be identified, based on their cycloheximide sensitivity and/or their resistance to aureobasidin A to which the transformants were sensitive. Therefore, the dual drug resistance of PGKp-YAP1 could be used as an effective selection for PGKp-YAP1 recipient cells. The PGKp-YAP1 ***marker*** was used to ***disrupt*** the LYS2 ***gene*** and to transform an industrial ***yeast*** strain, indicating that this ***marker*** can be used for efficient and reliable gene manipulations in any S. ***cerevisiae*** strain.
OSC.G 18 THERE ARE 18 CAPLUS RECORDS THAT CITE THIS RECORD (18 CITINGS)
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 24 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:914702 CAPLUS <<LOGINID::20110428>>
DN 136:364770
TI Meiotic recombination frequencies are affected by nutritional states in ***Saccharomyces*** ***cerevisiae***
AU Abdullah, Mohamad F. F.; Borts, Rhona H.
CS Department of Biochemistry, University of Oxford, Oxford, OX1 3QU, UK
SO Proceedings of the National Academy of Sciences of the United States of America (2001), 98(25), 14524-14529 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Meiotic recombination in the ***yeast*** ***Saccharomyces*** ***cerevisiae*** is initiated by programmed double-strand breaks at selected sites throughout the genome (hotspots). .alpha.-Hotspots are binding sites for transcription factors. Double-strand breaks at .alpha.-hotspots require binding of transcription factor but not high levels of transcription per se. We show that modulating the prodn. of the transcription factor Gcn4p by deletion or constitutive transcription alters the rate of gene conversion and crossing-over at HIS4. In addn., we show that alterations in the metabolic state of the cell change the frequency of gene conversion at HIS4 in a Gcn4p-dependent manner. We suggest that recombination data obtained from expts. using amino acid and other biosynthetic ***genes*** for ***gene*** ***disruptions*** and/or as genetic ***markers*** should be treated cautiously. The demonstration that Gcn4p affects transcription of more than 500 genes and that the recombinationally "hottest" ORFs tend to be Gcn4p-regulated suggest that the metabolic state of a cell, esp. with respect to nitrogen metab., is a determinant of recombination rates. This observation suggests that the effects of metabolic state may be global and may account for some as yet unexplained features of recombination in higher organisms, such as the differences in map length between the sexes.
OSC.G 33 THERE ARE 33 CAPLUS RECORDS THAT CITE THIS RECORD (33 CITINGS)
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 25 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:805130 CAPLUS <<LOGINID::20110428>>
DN 135:353755
TI Pichia farinosa orotidine-5'-phosphate decarboxylase gene URA3 as selectable marker for transformation
IN Suzuki, Chise; Kashiwagi, Yutaka; Kawasumi, Toshiyuki
PA Shokuhin Sogo Kenkyusho, Japan
SO Jpn. Kokai Tokkyo Koho, 7 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ---------- --------
PI JP 2001309784 A 20011106 JP 2000-132159 20000501
PRAI JP 2000-132159 20000501
AB A gene for orotidine-5'-phosphate (OMP) decarboxylase (URA3) from Pichia farinosa, plasmid vectors, and transformation of E. coli and ***Saccharomyces*** ***cerevisiae*** , are disclosed. Cloning of the gene with 81% homol. to ***Saccharomyces*** ***cerevisiae*** URA3 gene from Pichia farinosa KK1 strain (NFRI 3621) is described. S. ***cerevisiae*** W3031A strain transformed with the gene was capable of growing on uracil-deficient medium, indicating complementation of URA3 gene deficiency. Despite the URA3 complementation in S. ***cerevisiae*** , lack of homologous recombination makes it useful as selectable ***marker*** for ***gene*** ***disruption*** .

L11 ANSWER 26 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:688158 CAPLUS <<LOGINID::20110428>>
DN 135:299734
TI Endocrine disrupters - testing strategies to assess human hazard
AU Baker, V. A.
CS SEAC Toxicology Unit, Unilever Research, Colworth House, Sharnbrook, Bedfordshire, MK44 1LQ, UK
SO Toxicology in Vitro (2001), 15(4/5), 413-419 CODEN: TIVIEQ; ISSN: 0887-2333
PB Elsevier Science Ltd.
DT Journal
LA English
AB During the last decade, an hypothesis has been developed linking certain chems. (natural and synthetic) to obsd. and suspected adverse effects on reprodn. in both wildlife and humans. The issue of endocrine disruption originally focused on chems. that mimic the action of the natural hormone estrogen. However, the concern is now encompassing effects on the whole endocrine system. In response to public awareness, regulatory agencies (including the US EPA) and the OECD are formulating potential testing strategies and have begun the process of validating defined tests to systematically assess chems. for their endocrine-disrupting activities. In order to investigate chems. that have the potential to cause endocrine disruption, a large no. of in vitro and in vivo assays have been identified. In vitro test systems (particularly when used in combination) offer the possibility of providing an early screen for large nos. of chems. and can be useful in characterizing the mechanism of action and potency. In vitro assays in widespread use for the screening/characterization of endocrine-disrupting potential include hormone receptor ligand binding assays (detn. of the ability of a chem. to bind to the hormone receptor), cell proliferation assays (anal. of the ability of a chem. to stimulate the growth of estrogen-sensitive cells), reporter gene assays in ***yeast*** or mammalian cells (anal. of the ability of a chem. to stimulate the transcription of a reporter gene construct in cell culture), and the anal. of the regulation of endogenous estrogen-sensitive genes in cell lines. However, in vitro assays do not always reliably predict the outcome in vivo due to differences in metabolic capabilities of the test systems used and the diverse range of mechanisms by which endocrine-disrupting chems. may act. Therefore, a complementary battery of short- and long-term in vitro and in vivo assays (that assess both receptor and non-receptor-mediated mechanisms of action) seems the most appropriate way at present of assessing the potential endocrine-disrupting activities of chems. At Unilever, the authors have used a combination of in vitro assays (receptor binding, reporter gene, and cell proliferation assays) together with short-term in vivo tests (uterotrophic assay in immature rodents) to examine the estrogenic potential of a large no. of chems. An evaluation of the advantages and limitations of these methods is provided. Finally, any potential test system needs to be validated and standardized before the information generated can be for the identification of hazard, and possibly for risk assessment purposes.
OSC.G 78 THERE ARE 78 CAPLUS RECORDS THAT CITE THIS RECORD (78 CITINGS)

RE.CNT 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 27 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:618180 CAPLUS <<LOGINID::20110428>>
DN 135:191295
TI A dominant selectable ***marker*** , SAT, based on nourseothricin resistance for ***gene*** transformation and ***disruption*** in yeasts
IN Roemer, Terry; Bussey, Howard; Davison, John
PA McGill University, Can.
SO PCT Int. Appl., 35 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001061019 A2 20010823 WO 2001-CA194 20010219 WO 2001061019 A9 20020718 WO 2001061019 A3 20020926 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG US 20010031724 A1 20011018 US 2001-785669 20010216 US 6562595 B2 20030513 CA 2400534 A1 20010823 CA 2001-2400534 20010219
PRAI US 2000-183462P P 20000218 WO 2001-CA194 W 20010219
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The present invention provides a novel dominant selectable marker system in fungi that is based on the nucleoside-like antibiotic, nourseothricin (NST). This compd. possesses a powerful antifungal activity against Candida albicans and ***Saccharomyces*** ***cerevisiae*** . In particular, the present invention exploits the discovery of NST sensitivity in the pathogenic ***yeast*** , C. albicans, which leads to the development of a drug resistance ***marker*** useful in ***gene*** transformation and ***gene*** ***disruption*** expts. The present invention provides a genetically modified for expression in yeasts nourseothricin/streptothricin resistance gene (SAT) derived originally from the Escherichia coli SAT-1 (streptothricin acetyltransferase 1) gene. The modified SAT-1 gene has thymine at nucleotide position 441, instead of guanine, to encode leucine at amino acid position 147 according to the codon usage of C. albicans. The invention also provides the use of the naturally occurring nourseothricin acetyltransferase (NAT) from Streptomyces noursei. The present invention further provides a SAT expression module for gene knock-outs. The dominant selectable marker system of the invention facilitates: (1) gene manipulations in both clin. and exptl. relevant strains regardless of genotype and without affecting growth rate, or hyphal formation; and (2) antifungal drug discovery, including target validation and various forms of drug screening assays.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 28 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:577077 CAPLUS <<LOGINID::20110428>>
DN 136:211708
TI ***Yeast*** RNA polymerase I enhancer is dispensable for transcription of the chromosomal rRNA gene and cell growth, and its apparent transcription enhancement from ectopic promoters requires fob1 protein
AU Wai, Hobert; Johzuka, Katsuki; Vu, Loan; Eliason, Kristilyn; Kobayashi, Takehiko; Horiuchi, Takashi; Nomura, Masayasu
CS Department of Biological Chemistry, University of California-Irvine, Irvine, CA, 92697-1700, USA
SO Molecular and Cellular Biology (2001), 21(16), 5541-5553 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB At the end of the 35S rRNA gene within ribosomal DNA (rDNA) repeats in ***Saccharomyces*** ***cerevisiae*** lies an enhancer that has been shown to greatly stimulate rDNA transcription in ectopic reporter systems. However, that the enhancer is not necessary for normal levels of rRNA synthesis from chromosomal rDNA or for cell growth. ***Yeast*** strains which have the entire enhancer from rDNA deleted did not show any defects in growth or rRNA synthesis. The stimulatory activity of the enhancer for ectopic ***reporters*** is not obsd. in cells with ***disrupted*** nucleolar structures, suggesting that ***reporter*** ***genes*** are in general poorly accessible to RNA polymerase I (Pol I) machinery in the nucleolus and that the enhancer improves accessibility. A fob1 mutation abolishes transcription from the enhancer-dependent rDNA promoter integrated at the HIS4 locus without any effect on transcription from chromosomal rDNA. FOB1 is required for recombination hot spot (HOT1) activity, which also requires the enhancer region, and for recombination within rDNA repeats. Apparently, Fob1 protein stimulates interactions between rDNA repeats through the enhancer region, thus helping ectopic rDNA promoters to recruit the Pol I machinery normally present in the nucleolus.
OSC.G 29 THERE ARE 29 CAPLUS RECORDS THAT CITE THIS RECORD (29 CITINGS)
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 29 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:323115 CAPLUS <<LOGINID::20110428>>
DN 136:34478
TI Uncoupling ***yeast*** intron recognition from transcription with recursive splicing
AU Lopez, Pascal J.; Seraphin, Bertrand
CS EMBL, Heidelberg, D-69117, Germany
SO EMBO Reports (2000), 1(4), 334-339 CODEN: ERMEAX; ISSN: 1469-221X
PB Oxford University Press
DT Journal
LA English
AB Pre-mRNA splicing has to be coordinated with other processes occurring in the nucleus including transcription, mRNA 3' end formation and mRNA export. To analyze the relationship between transcription and splicing, the authors constructed a

network of nested introns. Introns were inserted in the 5' splice site and/or branchpoint of a synthetic ***yeast*** intron ***interrupting*** a ***reporter*** ***gene*** . The inserted introns mask the recipient intron from the cellular machinery until they are removed by splicing. Prodn. of functional mRNA from these constructs therefore requires recognition of a spliced RNA as a splicing substrate. The authors show that recurrent splicing occurs in a sequential and ordered fashion in vivo. Thus, in ***Saccharomyces*** ***cerevisiae*** , intron recognition and pre-spliceosome assembly is not tightly coupled to transcription.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 30 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:215979 CAPLUS <<LOGINID::20110428>>
DN 137:164214
TI GAPI, a novel selection and counter-selection ***marker*** for multiple ***gene*** ***disruptions*** in ***Saccharomyces*** ***cerevisiae*** . [Erratum to document cited in CA134:142393]
AU Regenberg, Birgitte; Hansen, Jorgen
CS Department of Yeast Genetics, Carlsberg Laboratory, Valby, DK-2500, Den.
SO Yeast (2001), 18(4), 389 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB On page 1113, column 2, lines 17-20 should read: "The direct repeats (DR1 and DR2) were derived from the Ashbya gossypii LEU2 (AgLEU2) gene and obtained by PCR amplification using plasmid pFA6-kanMX3....". Throughout the paper, "hisG" should read as "AgLEU2, "Salmonella typhimurium" as "Ashbya gossypii", and "hisG1" and "hisG2" as "DR1" and "DR2", resp.

L11 ANSWER 31 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:62270 CAPLUS <<LOGINID::20110428>>
DN 135:147896
TI Controlling gene expression in ***yeast*** by inducible site-specific recombination
AU Cheng, Tzu-Hao; Chang, Chuang-Rung; Joy, Prabha; Yablok, Svetlana; Gartenberg, Marc R.
CS Department of Pharmacology, Robert Wood Johnson Medical School, University of Medicine and Dentistry of New Jersey, Piscataway, NJ, 08854, USA
SO Nucleic Acids Research (2000), 28(24), e108/1-e108/6 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB An intron module was developed for ***Saccharomyces*** ***cerevisiae*** that imparts conditional gene regulation. The kanMX ***marker*** , flanked by loxP sites for the Cre recombinase, was embedded within the ACT1 intron and the resulting module was targeted to specific ***genes*** by PCR-mediated ***gene*** ***disruption*** . Initially, recipient genes were inactivated because the loxP-kanMX-loxP cassette prevented formation of mature transcripts. However, expression was restored by Cre-mediated site-specific recombination, which excised the loxP-kanMX-loxP cassette to generate a functional intron that contained a single loxP site. Cre recombinase activity was controlled at the transcriptional level by a GAL1::CRE expression vector or at the enzymic level by fusing the protein to the hormone-dependent regulatory domain of the estrogen receptor. Neg. selection against leaky pre-excision events was achieved by growing cells in modified minimal media that contained geneticin (G418). Advantages of this gene regulation technique, which we term the conditional knock-out approach, are that (i) modified genes are completely inactivated prior to induction, (ii) modified genes are induced rapidly to expression levels that compare to their unmodified counterparts, and (iii) it is easy to use and generally applicable.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 32 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:758691 CAPLUS <<LOGINID::20110428>>
DN 135:56656
TI Mis-targeting of multiple gene disruption constructs containing hisG
AU Davidson, John F.; Schiestl, Robert H.
CS Department of Cancer Cell Biology, Harvard School of Public Health, Boston, MA, 02115, USA
SO Current Genetics (2000), 38(4), 188-190 CODEN: CUGED5; ISSN: 0172-8083
PB Springer-Verlag
DT Journal
LA English
AB Gene targeting by homologous recombination occurs in ***Saccharomyces*** ***cerevisiae*** efficiently when there are as few as 30 base pairs of sequence homol. at both ends of the targeting construct. Multiple ***gene*** ***disruptions*** within a single cell are possible using the hisG cassette, which allows recovery of the ***marker*** but leaves a single hisG sequence imbedded in the ***disrupted*** ***gene*** (s). The authors use an integration hisG construct, which has limited homol. to the target at one end, to show that a single genomic copy of hisG decreases the percentage of integration at the target locus from 44% to 4.5% and two genomic hisG copies decrease it to less than 1%. Enlarging the homol. at the disruption construct abolishes this effect. Thus competition between endogenous hisG sequences and successive hisG cassette transformations occurs if there is limited homol. at one end of the targeting construct. Therefore, methods using limited homol., such as PCR-mediated gene targeting, are inefficient when significant internal homol. exists.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 33 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:690176 CAPLUS <<LOGINID::20110428>>
DN 134:142393
TI GAP1, a novel selection and counter-selection ***marker*** for multiple ***gene*** ***disruptions*** in ***Saccharomyces*** ***cerevisiae***
AU Regenberg, Birgitte; Hansen, Jorgen
CS Department of Yeast Genetics, Carlsberg Laboratory, Valby, DK-2500, Den.
SO Yeast (2000), 16(12), 1111-1119 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.

DT Journal
LA English
AB We report on the use of a new homologous marker for use in multiple gene deletions in S. ***cerevisiae*** , the general amino acid permease gene (GAP1). A GAP1 strain can utilize L-citrulline as the sole nitrogen source but cannot grow in the presence of the toxic amino acid D-histidine. L-citrulline as well as D-histidine uptake is mediated solely by the general amino acid permease, and a gap1 strain is therefore able to grow in the presence of D-histidine but cannot utilize L-citrulline. Gene disruption is effected by transforming a gap1 strain with a gene cassette generated by PCR, contg. GAP1 flanked by short (60 bp) stretches of the gene in question. Through homologous recombination, the cassette will integrate into the target gene, which is thus replaced by GAP1, and mutants are selected for on minimal L-citrulline medium. When propagated under non-selective conditions, some cells will lose the GAP1 gene. This is caused by recombination between two Salmonella typhimurium hisG direct repeats embracing GAP1, and will result in a sub-population of gap1 cells. Such cells are selected on a medium contg. D-histidine, and may subsequently be used for a second gene disruption. Hence, multiple gene disruptions can be made fast, cheaply and easily in a gap1 strain, with two pos. selection steps for each disruption.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 34 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:404882 CAPLUS <<LOGINID::20110428>>
DN 133:147419
TI Targeted gene disruption in Candida albicans wild-type strains: the role of the MDR1 gene in fluconazole resistance of clinical Candida albicans isolates
AU Wirsching, Stephanie; Michel, Sonja; Morschhauser, Joachim
CS Zentrum fur Infektionsforschung, Universitat Wurzburg, Wurzburg, D-97070, Germany
SO Molecular Microbiology (2000), 36(4), 856-865 CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell Science Ltd.
DT Journal
LA English
AB Resistance of the pathogenic ***yeast*** C. albicans to the antifungal agent fluconazole is often caused by active drug efflux out of the cells. In clin. C. albicans strains, fluconazole resistance frequently correlates with constitutive activation of the MDR1 gene, encoding a membrane transport protein of the major facilitator superfamily that is not expressed detectably in fluconazole-susceptible isolates. However, the mol. changes causing MDR1 activation have not yet been elucidated, and direct proof for MDR1 expression being the cause of drug resistance in clin. C. albicans strains is lacking as a result of difficulties in the genetic manipulation of C. albicans wild-type strains. A new strategy was developed for sequential ***gene*** ***disruption*** in C. albicans wild-type strains that is based on the repeated use of a dominant selection ***marker*** conferring resistance against mycophenolic acid upon transformants and its subsequent excision from the genome by FLP-mediated, site-specific recombination (MPAR-flipping). This mutagenesis strategy was used to generate homozygous mdr1/mdr1 mutants from 2 fluconazole-resistant clin. C. albicans isolates in which drug resistance correlated with stable, constitutive MDR1 activation. In both cases, disruption of the MDR1 gene resulted in enhanced susceptibility of the mutants against fluconazole, providing the 1st direct genetic proof that MDR1 mediates fluconazole resistance in clin. C. albicans strains. The new gene disruption strategy allows the generation of specific knock-out mutations in any C. albicans wild-type strain and therefore opens completely novel approaches for studying this most important human pathogenic fungus at the mol. level.
OSC.G 69 THERE ARE 69 CAPLUS RECORDS THAT CITE THIS RECORD (69 CITINGS)
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 35 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:290902 CAPLUS <<LOGINID::20110428>>
DN 133:219432
TI Intergenic complementation truncation mutants of cyclin-dependent kinase
AU Bitter, G. A.; Tsai, M.-M.; Putzke, A. P.; Leong, K.
CS Bit Tech Inc., Westlake Village, CA, 91361, USA
SO Molecular and General Genetics (2000), 263(2), 222-231 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB The ***Saccharomyces*** ***cerevisiae*** genes PHO80 and PHO85 encode, resp., a cyclin and cyclin-dependent kinase, which neg. regulate PHO5 gene transcription by phosphorylating the transcription activator Pho4p. Cyclin-dependent kinases (CDKs) are highly conserved proteins, both within and between species. It was previously demonstrated, using reporter genes activated in ***yeast*** by Pho4p, that hybrid proteins in which over two-thirds of Pho85p were replaced with the homologous region from human Cdk2 retained the function of native Pho85p with respect to promoter repression. In the present study, various truncated forms of the hybrid human- ***yeast*** CDKs were tested for function. Surprisingly, truncations in which significant portions of the C-terminal region of the 291-residue hybrid CDK were deleted retained activity. Genes encoding human Cdk2 proteins which terminated after amino acids 151, 140, 130, 120 and 90 each complement a chromosomal pho85 gene disruption in which the HIS3 gene is inserted at codon 49. Truncated Cdk2 proteins contg. less than 60 amino acids failed to complement the pho85::HIS3 gene disruption. Although the functional C-terminal truncations ***disrupt*** the ATP-binding and active sites of Cdk2, ***reporter*** ***gene*** repression mediated by these truncated proteins is apparently due to phosphorylation of Pho4p, since a gene in which the essential lysine codon at position 33 was converted to an arginine codon does not complement the chromosomal gene disruption. The human Cdk2 truncations were demonstrated to function through intergenic complementation. The intact Cdk2-Pho85 hybrid CDK complemented the pho85 mutation in ***yeast*** strains in which the entire PHO85 coding region was deleted from chromosome XVI. The C-terminal Cdk2 truncations, however, were non-functional in these strains and thus dependent for activity on the pho85 coding region which remained in the mutant pho85::HIS3 chromosomal locus. These genetic results are consistent with a model involving protein fragment complementation in which the active site of the CDK is bisected.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 36 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:233803 CAPLUS <<LOGINID::20110428>>
DN 133:172667
TI A novel multi-purpose cassette for repeated integrative epitope tagging of genes in ***Saccharomyces*** ***cerevisiae***
AU De Antoni, A.; Gallwitz, D.
CS Department of Molecular Genetics, Max-Planck-Institute for Biophysical Chemistry, Gottingen, D-37070, Germany
SO Gene (2000), 246(1-2), 179-185 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
AB Gene tagging can be achieved by homologous recombination in ***yeast*** . The kanr ***marker*** ***gene*** plays an important role in PCR-mediated ***gene*** ***disruption*** and PCR-mediated epitope tagging expts. In this paper, new modules contg. a tag-loxP-kanMX-loxP cassette are described that allow tagging of different genes by using the kanr marker repeatedly.
OSC.G 55 THERE ARE 55 CAPLUS RECORDS THAT CITE THIS RECORD (55 CITINGS)
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 37 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:18978 CAPLUS <<LOGINID::20110428>>
DN 132:318509
TI Long inverted repeats are an at-risk motif for recombination in mammalian cells
AU Waldman, Alan S.; Tran, Hiep; Goldsmith, Edie C.; Resnick, Michael A.
CS Department of Biological Sciences, University of South Carolina, Columbia, SC, 29208, USA
SO Genetics (1999), 153(4), 1873-1883 CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB Certain DNA sequence motifs and structures can promote genomic instability. We have explored instability induced in mouse cells by long inverted repeats (LIRs). A cassette was constructed contg. a herpes simplex virus thymidine kinase (tk) gene into which was inserted an LIR composed of two inverted copies of a 1.1-kb ***yeast*** URA3 gene sequence sepd. by a 200-bp spacer sequence. The tk gene was introduced into the genome of mouse Ltk- fibroblasts either by itself or in conjunction with a closely linked tk ***gene*** that was ***disrupted*** by an 8-bp XhoI linker insertion; rates of intrachromosomal homologous recombination between the ***markers*** were detd. Recombination between the two tk alleles was stimulated 5-fold by the LIR, as compared to a long direct repeat (LDR) insert, resulting in nearly 10-5 events per cell per generation. Of the tk+ segregants recovered from LIR-contg. cell lines, 14% arose from gene conversions that eliminated the LIR, as compared to 3% of the tk+ segregants from LDR cell lines, corresponding to a >20-fold increase in deletions at the LIR hotspot. Thus, an LIR, which is a common motif in mammalian genomes, is at risk for the stimulation of homologous recombination and possibly other genetic rearrangements.
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 38 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:749751 CAPLUS <<LOGINID::20110428>>
DN 132:77814
TI Effect of NAD+-dependent isocitrate dehydrogenase gene (IDH1, IDH2) disruption of sake ***yeast*** on organic acid composition in sake mash
AU Asano, Tadao; Kurose, Naotaka; Hiraoka, Nobutsugu; Kawakita, Sadao
CS Alcoholic Beverages Research Laboratories, Takara Shuzo Co. Ltd., Otsu, 520-2193, Japan
SO Journal of Bioscience and Bioengineering (1999), 88(3), 258-263 CODEN: JBBIF6; ISSN: 1389-1723
PB Society for Bioscience and Bioengineering, Japan
DT Journal
LA English
AB The ratio of org. acids in sake mash is a very important factor affecting the taste of alc. beverages. To alter the org. acid compn. in sake and investigate the mechanism of producing org. acids in sake mash, we examd. the effect of NAD+-dependent isocitrate dehydrogenase (IDH) activity deficiency in sake ***yeast*** by disrupting the IDH1 or IDH2 gene. Two haploid strains (MATa or MAT.alpha. genotype) isolated from sake ***yeast*** Kyokai no. 701 (K701) were ***disrupted*** using the aureobasidin A resistant ***gene*** (AUR1-C) as a selection ***marker*** . These disruptants were defective in the activity of IDH and failed to grow on medium contg. glycerol as a sole carbon source. Sake meter, alc. concn., and glucose consumption in sake brewed with the disruptants were reduced in comparison with those of the parental strains. The prodn. of citrate (including isocitrate), malate, and acetate by the disruptants was increased, but succinate prodn. was reduced to approx. half in comparison with the parental strains. These results indicate that approx. half the amt. of succinate in sake mash is produced via the oxidative pathway of the TCA cycle in sake ***yeast*** . While the diploid strain constructed by mating haploid disruptants for the IDH gene exhibited stronger fermn. ability than the haploid disruptants, almost similar profiles of components in sake were obtained for both strains.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 39 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:644390 CAPLUS <<LOGINID::20110428>>
DN 132:19289
TI One-step, PCR-mediated, gene disruption in the ***yeast*** Hansenula polymorpha
AU Gonzalez, Celedonio; Perdomo, German; Tejera, Paula; Brito, Nelida; Siverio, Jose M.
CS Departamento de Bioquimica y Biologia Molecular, Grupo del Metabolismo del Nitrogeno-Consejo Superior de Investigaciones Cientificas, Universidad de La Laguna, La Laguna, E-38206, Spain
SO Yeast (1999), 15(13), 1323-1329 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal

LA English
AB Previous evidence based on the experience of our lab. showed that one-step gene disruption in the ***yeast*** Hansenula polymorpha is not straightforward. A systematic study of several factors which could affect gene disruption frequency was carried out. We found that the more crit. factor affecting one-step ***gene*** ***disruption*** in H. polymorpha is the length of the target ***gene*** region flanking the ***marker*** gene. Target gene regions of about 1 kb flanking the ***marker*** ***gene*** were necessary to obtain a ***disruption*** frequency of about 50%. However, the gene ***marker*** , either homologous or heterologous, the locus and the strain examd. did not significantly affect the frequency of ***disruption*** ; the highest ***disruption*** frequency obtained for the YNR1 ***gene*** was in the strain HMI39, using the ***Saccharomyces*** ***cerevisiae*** URA3 gene as a ***marker*** . Since long regions flanking the gene ***marker*** do not allow the easy PCR-mediated strategies, developed for S. ***cerevisiae*** , to obtain constructs to ***disrupt*** a given ***gene*** in H. polymorpha, an alternative PCR strategy was developed.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 40 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:640011 CAPLUS <<LOGINID::20110428>>
DN 132:20912
TI Deletion of six open reading frames from the left arm of chromosome IV of ***Saccharomyces*** ***cerevisiae***
AU Tuller, Gabriele; Prein, Birgit; Jandrositz, Anita; Daum, Gunther; Kohlwein, Sepp D.
CS SFB Biomembrane Research Center and Institut fur Biochemie und Lebensmittelchemie, Technische Universitat Graz, Graz, A-8010, Austria
SO Yeast (1999), 15(12), 1275-1285 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB The construction of six deletion mutants of ***Saccharomyces*** ***cerevisiae*** and their basic phenotypic characterization are described. Open reading frames YDL148c, YDL109c, YDL021w, YDL019c, YDL018c and YDL015c from the left arm of chromosome IV were deleted using a polymerase chain reaction (PCR)-based ***disruption*** technique, introducing the kanMX4 resistance ***marker*** into the resp. ***genes*** . Gene replacement cassettes (pYORCs) for use in other strain backgrounds were cloned by PCR using DNA templates from haploid or diploid deletion mutants, and inserted into episomal plasmids. Cognate clones of all six ORFs were obtained by gap repair. Deletions were carried out in diploid cells and, after sporulation, yielded four viable spores for clones disrupted in YDL109c, YDL021w, YDL019c and YDL018c. Spores harboring disruptions in ORFs YDL148c and YDL015c germinated but underwent only a few divisions before ceasing growth, suggesting that the resp. genes are essential for vegetative growth on YPD complete media. The other deletion mutants grew like wild-type at different temps. and on different carbon sources. A brief computational anal. of the six ORFs studied in this work is presented.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 41 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:548749 CAPLUS <<LOGINID::20110428>>
DN 131:282173
TI Designer deletion and prototrophic strains derived from ***Saccharomyces*** ***cerevisiae*** strain W303-1a
AU Replogle, Kirstin; Hovland, Laura; Rivier, David H.
CS Department of Cell and Structural Biology, University of Illinois, Urbana, IL, 61801, USA
SO Yeast (1999), 15(11), 1141-1149 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB The authors report the construction of ***Saccharomyces*** ***cerevisiae*** strains isogenic to W303-1a that are designed to allow efficient genetic anal. To facilitate the generation of null alleles of target genes by PCR-mediated gene disruption, the authors constructed designer deletion alleles of the ARG4, TRP1 and URA3 genes. In addn., a single pair of oligonucleotide primers were designed that can be used to amplify any of several ***marker*** ***genes*** for use in PCR-mediated ***gene*** ***disruption*** . A new version of the "reusable" hisG-URA3-hisG cassette was constructed for use in PCR-mediated gene disruption. Finally, to facilitate the formation of isogenic diploids by selection, the authors constructed strains that contain combinations of wild-type alleles of ADE2, HIS3, LEU2, TRP1 and URA3.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 42 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:514243 CAPLUS <<LOGINID::20110428>>
DN 131:267778
TI Disruption of six open reading frames on chromosome X of ***Saccharomyces*** ***cerevisiae*** reveals a cluster of four essential genes
AU Esser, Karlheinz; Scholle, Bettina; Michaelis, Georg
CS Botanisches Institut, Heinrich-Heine-Universitat Dusseldorf, Dusseldorf, D-40225, Germany
SO Yeast (1999), 15(10B), 921-933 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB In this study we report the construction and basic phenotypic anal. of six ***Saccharomyces*** ***cerevisiae*** deletion mutants. The open reading frames (ORFs) YJL008C (gene symbol CCT8), YJL010C, YJL011C, YJL012C, YJL017W, and YJL020C from chromosome X have been ***disrupted*** by integration of deletion cassettes, comprising the bacterial KanMX4 ***marker*** ***gene*** and terminal long (LFH) or short (SFH) flanking sequences that are homologous to the 5' and 3' untranslated regions of the resp. ORFs. For correct disruption of ORF YJL008C, it was necessary to construct a deletion cassette flanked by 300-350 bp long target guide sequences by LFH-PCR. Transformations using ORF YJL008C gene disruption cassettes synthesized by std. SFH-PCR

exclusively resulted in false-pos. or multiple integration events, probably because seven addnl. genes homologous to CCT8 exist in the ***yeast*** genome. The other five ORFs have been disrupted using cassettes generated by SFH-PCR, comprising terminal homologous regions of approx. 50 bp to each target site. Correct genomic integration of the reporter modules was verified by anal. PCR and Southern hybridization. Deletion of YJL008C, YJL010C, YJL011C, and YJL012C was found to be lethal, as shown by sporulation and tetrad anal. This result is in contrast to the finding that only 16-20% of the genes in S. ***cerevisiae*** are estd. to be essential. The four essential genes described in this work are clustered, while the two other non-essential ORFs are sepd. by further ORFs. Although the two viable deletion mutants were tested against 60 different inhibitors, heavy metal ions and salts, no phenotype could be detected that co-segregated with the deletion during meiosis.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 43 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:412197 CAPLUS <<LOGINID::20110428>>
DN 131:182145
TI Unanticipated heterogeneity in growth rate and virulence among Candida albicans AAF1 null mutants
AU Rieg, Gunter; Fu, Yue; Ibrahim, Ashraf S.; Zhou, Xiang; Filler, Scott G.; Edwards, John E., Jr.
CS Division of Infectious Diseases, St. John's Cardiovascular Research Center, Department of Medicine, Harbor-UCLA Research and Education Institute, Torrance, CA, 90502, USA
SO Infection and Immunity (1999), 67(7), 3193-3198 CODEN: INFIBR; ISSN: 0019-9567
PB American Society for Microbiology
DT Journal
LA English
AB The disruption of a specific gene in Candida albicans is commonly used to det. the function of the gene product. The authors disrupted AAF1, a gene of C. albicans that causes ***Saccharomyces*** ***cerevisiae*** to flocculate and adhere to endothelial cells. They then characterized multiple heterozygous and homozygous mutants. These null mutants adhered to endothelial cells to the same extent as did the parent organism. However, mutants with presumably the same genotype revealed significant heterogeneity in their growth rates in vitro. This heterogeneity was not the result of the transformation procedure per se, nor was it caused by differences in the expression or function of URA3, a ***marker*** used in the process of ***gene*** ***disruption*** . The growth rate among the different heterozygous and homozygous null mutants was pos. correlated with in vivo virulence in mice. It is possible that the variable phenotypes of C. albicans were due to mutations outside of the AAF1 coding region that were introduced during the gene disruption process. These results indicate that careful phenotypic characterization of mutants of C. albicans generated through targeted gene disruption should be performed to exclude the introduction of unexpected mutations that may influence pathogenicity in mice.
OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 44 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:302560 CAPLUS <<LOGINID::20110428>>
DN 131:99725
TI Elevated growth of ***Saccharomyces*** ***cerevisiae*** ATH1 null mutants on glucose is an artifact of nonmatching auxotrophies of mutant and reference strains
AU Chopra, Rohini; Sharma, Vishva Mitra; Ganesan, K.
CS Institute of Microbial Technology, Chandigarh, 160 036, India
SO Applied and Environmental Microbiology (1999), 65(5), 2267-2268 CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB ***Yeast*** strains disrupted for ATH1, which encodes vacuolar acid trehalase, have been reported to grow to higher cell densities than ref. strains. We showed that the increase in cell d. is due to the URA3 ***gene*** introduced as a part of the ***disruption*** and concluded that the misinterpretation is a result of not using a control strain with matching auxotrophic ***markers*** .
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 45 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:237686 CAPLUS <<LOGINID::20110428>>
DN 131:83583
TI A 2-.mu.m DNA-based ***marker*** recycling system for multiple ***gene*** ***disruption*** in the ***yeast*** ***Saccharomyces*** ***cerevisiae***
AU Storici, Francesca; Coglievina, Maristella; Bruschi, Carlo V.
CS Microbiology Group, ICGEB, AREA Science Park, Trieste, I-34012, Italy
SO Yeast (1999), 15(4), 271-283 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB A mol. FRT (Flp recombinase recognition target)-based cassette system for multiple gene disruption in the ***yeast*** ***Saccharomyces*** ***cerevisiae*** was developed. FRT DNA sequences were designed with different core mutations and subsequently cloned in direct orientation upstream and downstream of a ***marker*** gene to serve as template for the amplification of a set of different ***gene*** ***disruption*** cassettes. After each disruption, the marker can be easily eliminated from its integration site by in vivo site-specific recombination between the two identical, mutated FRT sequences flanking the marker, leaving behind one FRT sequence with a particular point mutation. Since recombination between two FRTs with a different core mutation is extremely rare, the possibility of chromosome rearrangements, due to site-specific recombination between residual FRTs, is very low. In strains contg. 2-.mu.m ([cir+]) the site-specific reaction is catalyzed by the endogenous Flp gene product, whereas in strains without 2-.mu.m ([cir0]), the FLP gene is carried on the cassette, together with the marker gene. This system can be applied for haploid and diploid [cir+] and [cir0] strains.
OSC.G 37 THERE ARE 37 CAPLUS RECORDS THAT CITE THIS RECORD (37 CITINGS)

RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 46 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:204507 CAPLUS <<LOGINID::20110428>>
DN 131:54424
TI Rapid hypothesis testing with Candida albicans through gene disruption with short homology regions
AU Wilson, R. Bryce; Davis, Dana; Mitchell, Aaron P.
CS Department of Microbiology and Institute of Cancer Research, Columbia University, New York, NY, 10032, USA
SO Journal of Bacteriology (1999), 181(6), 1868-1874 CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB Disruption of newly identified genes in the pathogen Candida albicans is a vital step in detn. of gene function. Several ***gene*** ***disruption*** methods described previously employ long regions of homol. flanking a selectable ***marker*** . Here, we describe ***disruption*** of C. albicans ***genes*** with PCR products that have 50 to 60 bp of homol. to a genomic sequence on each end of a selectable ***marker*** . We used the method to disrupt two known genes, ARG5 and ADE2, and two sequences newly identified through the Candida genome project, HRM101 and ENX3. HRM101 and ENX3 are homologous to genes in the conserved RIM101 (previously called RIM1) and PacC pathways of ***Saccharomyces*** ***cerevisiae*** and Aspergillus nidulans. We show that three independent hrm101/hrm101 mutants and two independent enx3/enx3 mutants are defective in filamentation on Spider medium. These observations argue that HRM101 and ENX3 sequences are indeed portions of genes and that the resp. gene products have related functions.
OSC.G 347 THERE ARE 347 CAPLUS RECORDS THAT CITE THIS RECORD (348 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 47 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:615241 CAPLUS <<LOGINID::20110428>>
DN 129:340273
OREF 129:69217a,69220a
TI New constructs and strategies for efficient PCR-based gene manipulations in ***yeast***
AU Puig, Oscar; Rutz, Berthold; Luukkonen, B. G. Mattias; Kandels-Lewis, Stefanie; Bragado-Nilsson, Elisabeth; Seraphin, Bertrand
CS EMBL, Heidelberg, D-69117, Germany
SO Yeast (1998), 14(12), 1139-1146 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Gene disruption and tagging can be achieved by homologous recombination in the ***yeast*** genome. Several PCR-based methods have been described towards this end. However these strategies are often limited in their applications and/or their efficiencies and may be tech. demanding. Here we describe two plasmids for C-terminal tagging of proteins with the IgG binding domain of the Staphylococcus aureus protein A. We also present simple and reliable strategies based on PCR to promote efficient integration of exogenous DNA into the ***yeast*** genome. These simple methods are not limited to specific strains or ***markers*** and can be used for any application requiring homologous recombination such as ***gene*** ***disruption*** and epitope tagging. These strategies can be used for consecutive introduction of various constructs into a single ***yeast*** strain.
OSC.G 62 THERE ARE 62 CAPLUS RECORDS THAT CITE THIS RECORD (62 CITINGS)
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 48 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:537640 CAPLUS <<LOGINID::20110428>>
DN 129:312709
OREF 129:63733a,63736a
TI Identification of a novel .DELTA.6-acyl-group desaturase by targeted gene disruption in Physcomitrella patens
AU Girke, Thomas; Schmidt, Hermann; Zahringer, Ulrich; Reski, Ralf; Heinz, Ernst
CS Institut fur Allgemeine Botanik, Universitat Hamburg, Hamburg, D-22609, Germany
SO Plant Journal (1998), 15(1), 39-48 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB The moss Physcomitrella patens contains high levels of arachidonic acid. For its synthesis from linoleic acid by desatn. and elongation, novel .DELTA.5- and .DELTA.6- desaturases are required. To isolate one of these, PCR-based cloning was used, and resulted in the isolation of a full-length cDNA coding for a putatively new desaturase. The deduced amino acid sequence has 3 domains: a N-terminal segment of about 100 amino acids, with no similarity to any sequence in the data banks, followed by a cytochrome b5-related region and a C-terminal sequence with low similarity (27% identity) to acyl-lipid desaturases. To elucidate the function of this protein, we ***disrupted*** its ***gene*** by transforming P. patens with the corresponding linear genomic sequence, into which a pos. selection ***marker*** had been inserted. The mol. anal. of 5 transformed lines showed that the selection cartridge had been inserted into the corresponding genomic locus of all 5 lines. The gene disruption resulted in a dramatic alteration of the fatty acid pattern in the knockout plants. The large increase in linoleic acid and the concomitant disappearance of .gamma.-linolenic and arachidonic acid in all knockout lines suggested that the new cDNA coded for a .DELTA.6-desaturase. This was confirmed by expression of the cDNA in ***yeast*** and anal. of the resultant fatty acids by GC-MS. Only the transformed ***yeast*** cells were able to introduce a further double bond into the .DELTA.6-position of unsatd. fatty acids. This is the first report of a successful gene disruption in a multicellular plant resulting in a specific biochem. phenotype.
OSC.G 144 THERE ARE 144 CAPLUS RECORDS THAT CITE THIS RECORD (144 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 49 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:322012 CAPLUS <<LOGINID::20110428>>

DN 129:2617
OREF 129:639a,642a
TI Isolation and characterization of the temperature sensitive mutant of DNA repair gene RAD24 of ***Saccharomyces*** ***cerevisiae***
AU Zhu, Ying-Bao; Han, Yun; Fu, Xin; Tong, Tan-Jun
CS School of Clinical Medicine, Beijing Medical Univ., Beijing, 100083, Peop. Rep. China
SO Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao (1998), 14(2), 222-226 CODEN: ZSHXF2; ISSN: 1007-7626
PB Zhongguo Shengwu Huaxue Yu Fenzi Shengwu Xuebao Bianweihui
DT Journal
LA Chinese
AB The RAD24 gene of ***Saccharomyces*** ***cerevisiae*** is involved in a nucleotide excision repair. It encodes a protein of 268 amino acids. Deletion of this gene in genome is lethal. To study the function of RAD24 gene, the temp.-sensitive mutant of the gene was isolated by plasmid shuffling. First, the full length of wild type RAD24 gene was cloned into the YC-plac33 boned plasmid pRB363 which contains Ura3 gene, named pTS1 and transformed ***yeast*** HY684. Next, the Rad24 ***gene*** in genome of HY684 was deleted by one-step ***gene*** ***disruption*** in which the His3 ***gene*** ***marker*** was used. Then, the wild type RAD24 gene was cloned into YCplac22 boned plasmid pRB364 contg. Trp1 gene and treated with hydroxylamine to mutate the gene of interest and transformed HY684 contg. pTS1 plasmid. Trp+ Ura+ transformants were tested for temp. sensitive growth prior to transfer to medium contg. 5-FOA, which was selected for URA- cells, which lost the non-mutagenized RAD24 gene on the pRB364. This procedure eliminated any non-rad24 ts mutations. Finally, viability of the 5-FOA resistant Ura- Trp+ cells could only be due to the presence of the mutagenized pRB364 plasmid and a rad24-ts3 mutant was obtained by screening replicating plates, UV-survival test indicates that the mutant was highly sensitive to UV, and its synthesis of DNA, RNA and protein was much decreased compared with the wild type strain.

L11 ANSWER 50 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:165107 CAPLUS <<LOGINID::20110428>>
DN 128:304509
OREF 128:60229a,60232a
TI Transformation system for prototrophic industrial yeasts using the AUR1 gene as a dominant selection marker
AU Hashida-Okado, Takashi; Ogawa, Atsuko; Kato, Ikunoshin; Takesako, Kazutoh
CS Otsu, 3-4-1 Seta, Biotechnology Research Laboratories, Takara Shuzo Co., Ltd., Shiga, 520-21, Japan
SO FEBS Letters (1998), 425(1), 117-122 CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB We show a new transformation system for prototrophic ***yeast*** strains including those of ***Saccharomyces*** ***cerevisiae*** , Kluyveromyces lactis, K. marxianus, and Candida glabrata. This system is composed of an antibiotic, aureobasidin A (AbA), and its resistance gene AUR1-C as a selection marker. Southern anal. of genomic DNAs of the transformants indicated that the copy no. of the plasmid increased from one to more than four, depending on the concn. of AbA used for selection of the transformants. The AUR1-C ***gene*** was also effective as a selection ***marker*** for ***gene*** ***disruption*** , and was able to ***disrupt*** both copies of the ***gene*** on homologous chromosomes of diploid cells by a single round of transformation. This system has a broad application in the transformation and gene disruption of prototrophic strains of a variety of ***yeast*** species.
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 51 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:122199 CAPLUS <<LOGINID::20110428>>
DN 128:241639
OREF 128:47785a,47788a
TI Isoenzyme function of n-alkane-inducible cytochromes P450 in Candida maltosa revealed by sequential gene disruption
AU Ohkuma, Moriya; Zimmer, Thomas; Iida, Toshiya; Schunck, Wolf-Hagen; Ohta, Akinori; Takagi, Masamichi
CS Laboratory of Cellular Genetics, Department of Biotechnology, The University of Tokyo, Tokyo, 113, Japan
SO Journal of Biological Chemistry (1998), 273(7), 3948-3953 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB An n-alkane-assimilating ***yeast*** , Candida maltosa, contains multiple n-alkane-inducible forms of cytochromes P 450 (P450alk), which can be assumed to catalyze terminal hydroxylation of n-alkanes in the assimilation pathway. Eight structurally related P450alk genes have been identified. In the present study, the function of four major isoforms of P450alk (encoded by ALK1, ALK2, ALK3, and ALK5 genes) was investigated by sequential gene disruption. Auxotrophic ***markers*** used for the selection of disrupted strains were regenerated repeatedly through either mitotic recombination between heterozygous alleles of the diploid genome or directed deletion of the ***marker*** ***gene*** , to allow sequential ***gene*** ***disruptions*** within a single strain. The strain depleted of all four isoforms could not utilize n-alkanes for growth, providing direct evidence that P450alk is essential for n-alkane assimilation. Growth properties of a series of intermediate disrupted strains, plasmid-based complementation, and enzyme assays after heterologous expression of single isoforms revealed (i) that each of the four individual isoforms is alone sufficient to allow growth on long chain n-alkane, (ii) that the ALK1-encoding isoform is the most versatile and efficient P450alk form, considering both its enzymic activity and its ability to confer growth on n-alkanes of different chain length, and (iii) that the ALK5-encoding isoform exhibits a rather narrow substrate specificity and thus cannot support the utilization of short chain n-alkanes.
OSC.G 40 THERE ARE 40 CAPLUS RECORDS THAT CITE THIS RECORD (40 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 52 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:109749 CAPLUS <<LOGINID::20110428>>
DN 128:239980
OREF 128:47397a,47400a

TI PCR- and ligation-mediated synthesis of ***marker*** cassettes with long flanking homology regions for ***gene*** ***disruption*** in ***Saccharomyces*** ***cerevisiae***
AU Nikawa, Jun-ichi; Kawabata, Machiko
CS Department of Biochyemical Engineering and Science, Faculty of Computer Science and Systems Engineering, Kyushu Inst. of Technology, Fukuoka, 820, Japan
SO Nucleic Acids Research (1998), 26(3), 860-861 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB We developed a novel method for synthesizing ***marker*** - ***disrupted*** alleles of ***yeast*** ***genes*** . The first step is PCR amplification of two sequences located upstream and downstream of the reading frame to be disrupted. Due to the addn. of non-specific single A overhangs by Taq DNA polymerase, each PCR product can be ligated with a marker DNA which has T residues at its 3' ends. After amplification of individual ligation products through the second PCR, both products are mixed and annealed, and the single strand is converted to a double strand by an extension reaction. The final step is PCR amplification of the fragment composed of a selectable marker and two flanking sequences with the outermost primers. This method is rapid and needs only short oligonucleotides as primers.
OSC.G 43 THERE ARE 43 CAPLUS RECORDS THAT CITE THIS RECORD (43 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 53 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:90802 CAPLUS <<LOGINID::20110428>>
DN 128:228371
OREF 128:45193a,45196a
TI Designer deletion strains derived from ***Saccharomyces*** ***cerevisiae*** S288C: a useful set of strains and plasmids for PCR-mediated gene disruption and other applications
AU Brachmann, Carrie Baker; Davies, Adrian; Cost, Gregory J.; Caputo, Emerita; Li, Joachim; Hieter, Philip; Boeke, Jef D.
CS Dep. Molecular Biology and Genetics, Johns Hopkins Univ. Sch. Med., Baltimore, MD, 21205, USA
SO Yeast (1998), 14(2), 115-132 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB A set of ***yeast*** strains based on ***Saccharomyces*** ***cerevisiae*** S288C in which commonly used selectable marker genes are deleted by design based on the ***yeast*** genome sequence has been constructed and analyzed. These strains minimize or eliminate the homol. to the corresponding marker genes in commonly used vectors without significantly affecting adjacent gene expression. Because the homol. between commonly used auxotrophic marker gene segments and genomic sequences has been largely or completely abolished, these strains will also reduce plasmid integration events which can interfere with a wide variety of mol. genetic applications. We also report the construction of new members of the pRS400 series of vectors, contg. the kanMX, ADE2 and MET15 genes.
OSC.G 1012 THERE ARE 1012 CAPLUS RECORDS THAT CITE THIS RECORD (1014 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 54 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:30616 CAPLUS <<LOGINID::20110428>>
DN 128:138446
OREF 128:27143a,27146a
TI Transient inhibition of histone deacetylation alters the structural and functional imprint at fission ***yeast*** centromeres
AU Ekwall, Karl; Olsson, Tim; Turner, Bryan M.; Cranston, Gwen; Allshire, Robin C.
CS MRC Human Genetics Unit, Western General Hospital, Edinburgh, EX4 2XU, UK
SO Cell (Cambridge, Massachusetts) (1997), 91(7), 1021-1032 CODEN: CELLB5; ISSN: 0092-8674
PB Cell Press
DT Journal
LA English
AB Histone acetylation may act to mark and maintain transcriptionally active or inactive chromosomal domains through the cell cycle and in different lineages. A novel role for histone acetylation in centromere regulation has been identified. Exposure of fission ***yeast*** cells to Trichostatin A (TSA), a specific inhibitor of histone deacetylase, interferes with repression of ***marker*** ***genes*** in centromeric heterochromatin, causes chromosome loss, and ***disrupts*** the localization of Swi6p, a component of centromeric heterochromatin. Transient TSA treatment induces a heritable hyperacetylated state in centromeric chromatin that is propagated in lineages in the absence of drug. This state is linked in cis to the treated centromere locus and correlates with inheritance of functionally defective centromeres and persistent chromosome segregation problems. Thus, assembly of fully functional centromeres is partly imprinted in the underacetylated or transcriptionally silent state of centromeric chromatin.
OSC.G 246 THERE ARE 246 CAPLUS RECORDS THAT CITE THIS RECORD (246 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 55 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1997:600409 CAPLUS <<LOGINID::20110428>>
DN 127:288899
OREF 127:56321a,56324a
TI Disruption of six novel ***yeast*** genes reveals three genes essential for vegetative growth and one required for growth at low temperature
AU Huang, Meng-Er; Cadieu, Edouard; Souciet, Jean-Luc; Galibert, Francis
CS Lab. Biochimie Biologie Moleculaire, Faculte Medecine, UPR41 CNRS 'Recombinaisons Genetiques', Rennes, 35043, Fr.
SO Yeast (1997), 13(12), 1181-1194 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB We describe here the construction of six deletion mutants and their basic phenotypic anal. Six open reading frames (ORFs) from chromosome X, YJR039w, YJR041c, YJR043c, YJR046w,

YJR053w and YJR065c, were disrupted by deletion cassettes with long (LFH) or short (SFH) flanking regions homologous to the target locus. The LFH deletion cassette was made by introducing into the kanMX4 marker module two polymerase chain reaction (PCR) fragments several hundred base pairs (bp) in size homologous to the promoter and terminator regions of a given ORF. The SFH ***gene*** ***disruption*** construct was obtained by PCR amplification of the kanMX4 ***marker*** with primers providing homol. to the target gene. The region of homol. to mediate homologous recombination was about 70 bp. Sporulation and tetrad anal. revealed that ORFs YJR041c, YJR046w and YJR065c are essential genes. Complementation tests by corresponding cognate gene clones confirmed this observation. The non-growing haploid segregants were obsd. under the microscope. The yjr041c.DELTA. haploid cells gave rise to microcolonies comprising about 20 to 50 cells. Most yjr046w.DELTA. cells were blocked after one or two cell cycles with heterogeneous bud sizes. The yjr065c.DELTA. cells displayed an unbudded spore or were arrested before completion of the first cell division cycle with a bud of variable size. The deduced protein of ORF YJR065c, that we named Act4, belongs to the Arp3 family of actin-related proteins. Three other ORFs, YJR039w, YJR043c and YJR053w are non-essential genes. The yjr043c.DELTA. cells hardly grew at 15.degree.C, indicating that this gene is required for growth at low temp. Complementation tests confirmed that the disruption of YJR043c is responsible for this growth defect. In addn., the mating efficiency of yjr043c.DELTA. and yjr053w.DELTA. cells appear to be moderately affected.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 56 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1997:431221 CAPLUS <<LOGINID::20110428>>
DN 127:105823
OREF 127:20303a,20306a
TI RNA binding analysis of ***yeast*** REF2 and its two-hybrid interaction with a new gene product, FIR1
AU Russnak, Roland; Pereira, Shalini; Platt, Terry
CS Department of Biochemistry and Biophysics, University of Rochester Medical Center, Rochester, NY, 14642, USA
SO Gene Expression (1997), Volume Date 1996, 6(4), 241-258 CODEN: GEEXEJ; ISSN: 1052-2166
PB Cognizant Communication Corp.
DT Journal
LA English
AB The product of the REF2 gene is required for optimal levels of endonucleolytic cleavage at the 3' ends of ***yeast*** mRNA, prior to the addn. of a poly(A) tail. To test the role of the previously demonstrated nonspecific affinity of REF2 for RNA in this process, the authors have identified RNA binding mutants in vitro and tested them for function within the cell. One REF2 variant, with an internal deletion of 82 amino acids (269-350), displays a 10-fold redn. in RNA binding, yet still retains full levels of processing activity in vivo. Conversely, a series of carboxyl-terminal deletions that maintain full RNA binding capability have progressively decreasing activity. These results rule out a major role for the central RNA binding domain of REF2 in mRNA 3' end processing and demonstrate the importance of the carboxyl-terminal region. To ask if the stimulatory role of REF2 depends on interactions with other proteins, the authors used a two-hybrid screen to identify a new protein termed FIR1 (Factor Interacting with REF) encoded on chromosome V. FIR1 interacts with two independent regions of REF2, one of which (amino acids 268-345) overlaps the RNA binding domain and is dispensable for REF2 function, whereas the other (amino acids 391-533) is located within the crit. carboxyl-terminus. As with REF2, FIR1 has a small but detectable role in influencing the efficiency of poly(A) site use. ***Yeast*** strains contg. a ***disrupted*** FIR1 ***gene*** are slightly less efficient in the use of cryptic poly(A) sites located within the lacZ portion of an ACTY1-lacZ ***reporter*** construct. Likewise, a double .DELTA.ref2, .DELTA.fir1 mutant is more defective in processing of a reporter CYC1 poly(A) site than .DELTA.ref2 alone. This synergistic response provides addnl. support for the interaction of FIR1 with REF2 in vivo, and suggests that a no. of gene products may be involved in regulating the cleavage reaction in ***yeast*** .
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 57 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1997:411133 CAPLUS <<LOGINID::20110428>>
DN 127:61334
OREF 127:11621a,11624a
TI 'Marker Swap' plasmids: convenient tools for budding ***yeast*** molecular genetics
AU Cross, Frederick R.
CS Rockefeller Univ., New York, NY, 10021, USA
SO Yeast (1997), 13(7), 647-653 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB One-step ***gene*** ***disruption*** constructs for ***disruption*** of HIS3, LEU2, TRP1 or URA3 with each of the other three ***markers*** have been constructed. All of these constructs have been tested and found to effectively convert ***markers*** either in ***gene*** ***disruptions*** or on plasmids. The 'swapped' strains allow the unambiguous genetic anal. of synthetic phenotypes with multiple ***genes*** , even if the original ***gene*** ***disruptions*** were made with the same ***marker*** . They also allow introduction of multiple plasmids in a single transformant, even if the original plasmids had the same ***marker*** , and allow transformation of plasmids into strains contg. ***gene*** ***disruptions*** made with the same ***marker*** that is on the plasmids. These 'marker-swap' plasmids therefore eliminate the need for much subcloning to change markers. Marker-swapped alleles are acceptably stable mitotically and meiotically for most applications.
OSC.G 120 THERE ARE 120 CAPLUS RECORDS THAT CITE THIS RECORD (120 CITINGS)

L11 ANSWER 58 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1997:373030 CAPLUS <<LOGINID::20110428>>
DN 127:76692
OREF 127:14541a,14544a
TI Cassette for the generation of sequential gene disruptions in the ***yeast*** Schizosaccharomyces pombe
AU McNabb, David S.; Pak, Sally M.; Guarente, Leonard
CS Massachusetts Inst. Technol., Cambridge, MA, USA

SO BioTechniques (1997), 22(6), 1134-1139 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton
DT Journal
LA English
AB The ability to conveniently construct gene disruptions is an important methodol. for genetic anal. of the fission ***yeast*** Schizosaccharomyces pombe. Because of the limited no. of selectable ***markers*** available for generating ***gene*** ***disruptions*** in fission ***yeast*** , the construction of strains that contain multiple ***gene*** ***disruptions*** can be quite difficult. This becomes a particular problem when episomal plasmids carrying selectable markers are also required within the same strains. To alleviate these difficulties, we have constructed a hisG-ura4+-hisG cassette that can be used repeatedly for constructing gene disruptions in S. pombe. This cassette allows the recycling of the ura4+ ***marker*** , thereby permitting the ***disruption*** of an indefinite no. of ***genes*** sequentially within the same strain and/or for subsequently introducing a ura4+-marked plasmid.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 59 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1997:198887 CAPLUS <<LOGINID::20110428>>
DN 126:273178
OREF 126:52841a,52844a
TI ORF7 of ***yeast*** plasmid pGKL2: analysis of gene expression in vivo
AU Schaffrath, Raffael; Meinhardt, Friedhelm; Meacock, Peter A.
CS Dep, Genetics, Univ. Leicester, Leicester, LE1 7RH, UK
SO Current Genetics (1997), 31(2), 190-192 CODEN: CUGED5; ISSN: 0172-8083
PB Springer
DT Journal
LA English
AB ORF7 of Kluyveromyces lactis killer plasmid pGKL2 (k2) is capable of encoding a putative RNA polymerase subunit of 16 kDa. RNA anal. detected a single, plasmid-dependent ORF7 transcript of 550 nt indicating that the gene is transcribed mono-cistronically. Attempted one-step ***gene*** ***disruption*** of ORF7 resulted in chromosomal integration of the ***marker*** ***gene*** rather than the formation of stable recombinant k2ORF70 deletion plasmids. Thus, ORF7 appears to be a potential cis-dominant locus the integrity of which is indispensable for plasmid stability. The ORF7 gene product was over-produced as a c-myc-tagged fusion protein in Escherichia coli. Western-blot anal. of total ***yeast*** protein exts. using an antibody against this Orf7-c-myc fusion product identified a protein band with an apparent mol. wt. of 17 kDa. This protein corresponds in size to the predicted product and is only detectable in plasmid-carrying killer yeasts.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)

L11 ANSWER 60 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1997:197176 CAPLUS <<LOGINID::20110428>>
DN 126:260074
OREF 126:50253a,50256a
TI The ***Saccharomyces*** ***cerevisiae*** MADS-box transcription factor Rlm1 is a target for the Mpk1 mitogen-activated protein kinase pathway
AU Dodou, Evdokia; Treisman, Richard
CS Transcription Laboratory, ICRF Laboratories, London, WC2A 3PX, UK
SO Molecular and Cellular Biology (1997), 17(4), 1848-1859 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB Mutation of ***Saccharomyces*** ***cerevisiae*** RLM1, which encodes a MADS-box transcription factor, confers resistance to the toxic effects of constitute activity of the Mpk1 mitogen-activated kinase (MAPK) pathway. The Rlm1 DNBA-binding domain, which is similar to that of the metazoan MEF2 transcription factors, is also closely related to that of a second S. ***cerevisiae*** protein, Smp1 (second MEF2-like protein), encoded by the YBR182C open reading frame (N. Demolis et al., ***Yeast*** 10:1511-1525, 1994; H. Feldmann et al., EMBO J. 13:5795-5809, 1994). We show that Rlm1 and Smp1 have MEF2-related DNA-binding specificities: Rlm1 binds with the same specificity as MEF2, CTA(T/A)4TAG, while SMP1 binds a more extended consensus sequence, ACTACTA(T/A)4TAG. The two DNA-binding domains can heterodimerize with each other and with MEF2A. Deletion of RLM1 enhances resistance to cell wall ***disruptants*** , increases satn. d., reduces flocculation, and inactivates ***reporter*** ***genes*** controlled by the Rlm1 consensus binding site. Deletion of SMP1 neither causes these phenotypes nor enhances the Rlm1 deletion phenotype. However, overexpression of the DNA-binding domain of either protein causes an osmoremedial phenotype. Synthetic and naturally occurring MEF2 consensus sequences exhibit strong RLM1- and MPK1-dependent upstream activation sequence activity. Transcriptional activation by Rlm1 requires its C-terminal sequences, and Gal4 fusion proteins contg. Rlm1 C-terminal sequences to act as MPK1-dependent transcriptional activators. These results establish the Rlm1 C-terminal sequences as a target for the Mpk1 MAPK pathway.
OSC.G 107 THERE ARE 107 CAPLUS RECORDS THAT CITE THIS RECORD (107 CITINGS)

L11 ANSWER 61 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1997:81833 CAPLUS <<LOGINID::20110428>>
DN 126:127517
OREF 126:24533a,24536a
TI Expression of a ***reporter*** ***gene*** ***interrupted*** by the Candida albicans group I intron is inhibited by base analogs
AU mercure, Stephane; Cousineau, Linda; Montplaisir, Serge; Belhumeur, Pierre; Lemay, Guy
CS Dep. de Microbiologie et Immunologie, Univ. de Montreal, Montreal, QC, H3C 3J7, Can.
SO Nucleic Acids Research (1997), 25(2), 431-437 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB We previously reported the identification of an intron (CaLSU) in the 25S rRNA of some Candida albicans ***yeast*** strains. CaLSU was shown to self-splice and has the potential to adopt a secondary structure typical of group I introns. The presence of CaLSU in C. albicans strains correlates with a high degree of susceptibility to base analog antifungal agents, 5-fluorocytosine (5-FC) or 5-fluorouracil (5-FU). Cell death,

resulting from addn. to base analogs to growing cultures, precluded demonstration of a causal relationship between CaLSU presence and susceptibility to base analogs. In the present study, CaLSU was inserted in a non-essential lacZ reporter gene and expression was examd. in ***Saccharomyces*** ***cerevisiae*** . Different mutations affecting in vitro self-splicing also had similar effects on reporter gene expression in vivo. This indicates that in vivo removal of CaLSU from the reporter gene occurs through the typical self-splicing mechanism of group I introns. Base analogs inhibited expression of the reporter gene product in a concn.-dependent manner upon their addn. to the cultures. This supports a model in which disruption of intron secondary structure, consecutive to the incorporation of nucleotide analogs, is a major factor detg. the susceptibility of C.albicans cells to base analogs.
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)

L11 ANSWER 62 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:725951 CAPLUS <<LOGINID::20110428>>
DN 126:43277
OREF 126:8437a,8440a
TI New vectors for combinatorial deletions in ***yeast*** chromosomes and for gap-repair cloning using 'split-marker' recombination
AU Fairhead, Cecile; Llorente, Bertrand; Denis, Francoise; Soler, Maria; Dujon, Bernard
CS Unite Genetique Moleculaire Levures, Inst. Pasteur, Paris, F-75724, Fr.
SO Yeast (1996), 12(14), 1439-1457 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB New tools are needed for speedy and systematic study of the numerous genes revealed by the sequence of the ***yeast*** genome. We have developed a novel transformation strategy, based on 'split-marker' recombination, which allows generation of chromosomal deletions and direct gene cloning. For this purpose, pairs of ***yeast*** vectors have been constructed which offer a no. of advantages for large-scale applications such as one-step cloning of target sequence homologs and combinatorial use. Gene deletions or gap-repair clonings are obtained by cotransformation of ***yeast*** by a pair of recombinant plasmids. Gap-repair vectors are based on the URA3 marker. Deletion vectors include the URA3, LYS2 and kanMX selection markers flanked by I-SceI sites, which allow their subsequent elimination from the transformant without the need for counter-selection. The application of the 'split-marker' vectors to the anal. of a few open reading frames of chromosome XI is described.
OSC.G 87 THERE ARE 87 CAPLUS RECORDS THAT CITE THIS RECORD (87 CITINGS)

L11 ANSWER 63 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:621117 CAPLUS <<LOGINID::20110428>>
DN 125:266908
OREF 125:49617a,49620a
TI Efficient selection of hygromycin-B-resistant Yarrowia lipolytica transformants
AU Corder Otero, R.; Gaillardin, C.
CS Institut National Agronomique Paris-Grignon, Centre Biotechnologies Agro-Industrielles, Thiverval-Grignon, F-78850, Fr.
SO Applied Microbiology and Biotechnology (1996), 46(2), 143-148 CODEN: AMBIDG; ISSN: 0175-7598
PB Springer
DT Journal
LA English
AB The ***yeast*** Yarrowia lipolytica was shown to be sensitive to the aminoglycoside antibiotic hygromycin B. Spontaneous resistants appeared at a frequency of (2-5) .times. 10-7 in media contg. 100 mg/L drug. In order to develop a new selective marker for the transformation of this ***yeast*** , we constructed new plasmids expressing the Escherichia coli hygromycin-resistance gene (hph) under the control of the promoter and terminator sequences of the strongly expressed XPR2 gene of Y. lipolytica. Direct selection of hygromycin-B-resistant transformants on complete medium was very efficient and resulted in transformation frequencies comparable to those obsd. with conventional auxotrophic markers. This new ***marker*** can be used for integrating single copies of plasmid and for ***gene*** ***disruption*** and provides a convenient tag for genetic studies.

L11 ANSWER 64 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:475393 CAPLUS <<LOGINID::20110428>>
DN 125:134040
OREF 125:24905a,24908a
TI Rapid method for construction of gene disruption plasmids in ***Saccharomyces*** ***cerevisiae***
AU Fujimura, Hiro-aki
CS Hoechst Japan Limited, Kawagoe, Japan
SO BioTechniques (1996), 21(2), 208-209 CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton
DT Journal
LA English
AB As the first step to elucidate the function of cloned genes, gene disruption is an essential and direct approach to clarify the biol. role of target genes. The gene disruption technique was originally established by using chromosomal integration, and was improved as a one-step gene replacement. The improved method usually involves purifn. of a DNA fragment, which is used for disruption of the cloned genes. Here, the author describes an improved and rapid method that does not need any purifn. of DNA fragments for ***marker*** ***genes*** to construct ***gene*** ***disruption*** plasmids.

L11 ANSWER 65 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:465964 CAPLUS <<LOGINID::20110428>>
DN 125:133925
OREF 125:24885a,24888a
TI Sticky-end polymerase chain reaction method for systematic gene disruption in ***Saccharomyces*** ***cerevisiae***
AU Maftahi, M.; Gaillardin, C.; Nicaud, J.-M.
CS Inst. National Agronomique Paris-Grignon, Lab. Genetique Moleculaire Cellulaire, Thiverval-Grignon, 78850, Fr.
SO Yeast (1996), 12(9), 859-868 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB We describe a new procedure for the generation of plasmids contg. a large promoter and terminator region of a gene of interest, useful for gene disruption. In a two-step polymerase chain reaction (PCR), a fragment, corresponding to the terminator and promoter regions sepd. by a 16 bp sequence

contg. a rare restriction site (e.g. AscI), is synthesized (T-P fragment). This PCR fragment is cloned in vectors presenting a rare blunt-end cloning site and a ***yeast*** marker for selection in ***Saccharomyces*** ***cerevisiae*** (TRP1, HIS3 and KanMX). The final plasmids are used directly for gene disruption after linearization by the enzyme (e.g. AscI) specific for the rare restriction site. This approach was used to disrupt three open reading frames identified during the sequencing of clone COS14-1 from chromosome XIV of S. ***cerevisiae*** .
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

L11 ANSWER 66 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:448036 CAPLUS <<LOGINID::20110428>>
DN 125:134021
OREF 125:24905a
TI A new efficient gene disruption cassette for repeated use in budding ***yeast***
AU Gueldener, Ulrich; Heck, Susanne; Fiedler, Thomas; Beinhauer, Jens; Hegemann, Johannes H.
CS Institut Mikrobiologie Molekularbiologie, Justus-Liebig-Universitaet Giessen, Giessen, 35392, Germany
SO Nucleic Acids Research (1996), 24(13), 2519-2524 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The dominant kanr ***marker*** ***gene*** plays an important role in ***gene*** ***disruption*** expts. in budding ***yeast*** , as this ***marker*** can be used in a variety of ***yeast*** strains lacking the conventional ***yeast*** ***markers*** . We have developed a loxP-kanMX-loxP ***gene*** ***disruption*** cassette, which combines the advantages of the heterologous kanr ***marker*** with those from the Cre-lox P recombination system. This disruption cassette integrates with high efficiency via homologous integration at the correct genomic locus (routinely 70%). Upon expression of the Cre recombinase, the kanMX module is excised by an efficient recombination between the loxP sites, leaving behind a single loxP site at the chromosomal locus. This system allows repeated use of the kanr marker gene and will be of great advantage for the functional anal. of gene families.
OSC.G 34 THERE ARE 34 CAPLUS RECORDS THAT CITE THIS RECORD (34 CITINGS)

L11 ANSWER 67 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:295408 CAPLUS <<LOGINID::20110428>>
DN 124:334111
OREF 124:61789a,61792a
TI PCR-based gene disruption in ***Saccharomyces*** ***cerevisiae***
AU Smith, Julianne; Zou, Hui; Rothstein, Rodney
CS Dep. Genetics, Columbia Univ., New York, NY, 10032, USA
SO Methods in Molecular and Cellular Biology (1996), Volume Date 1994-1995, 5(5), 270-277 CODEN: MMCBEV; ISSN: 0898-7750
PB Wiley
DT Journal
LA English
AB Gene disruption is a powerful method for manipulating the ***yeast*** genome. This technique involves inactivation of an endogenous gene by transforming the cell with a linear DNA fragment modified in vitro. The fragment is engineered so that a selectable marker is flanked by sequences of the gene of interest, which direct homologous recombination into the genome. Recently, polymerase chain reaction (PCR) technol. has been used to facilitate the generation of gene disruption fragments, allowing the precise addn. and/or deletion of sequences. In this report, we describe three PCR-based gene disruption strategies. In the first, a marked ***gene*** ***disruption*** fragment is generated by using PCR primers that contain sequences homologous to the targeting gene and the selectable ***marker*** . After PCR amplification, the product can be directly transformed into the cell to generate a marked disruption. In the second method, an unmarked deletion is created by utilizing a short PCR product that contains only sequences flanking the target gene. In the third method, primers can be designed to generate a disruption fragment contg. a selectable marker flanked by direct repeats. In this method, subsequent loss of the marker by direct repeat recombination results in an unmarked deletion.

L11 ANSWER 68 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:158443 CAPLUS <<LOGINID::20110428>>
DN 124:222060
OREF 124:40909a,40912a
TI PCR-synthesis of ***marker*** cassettes with long flanking homology regions for ***gene*** ***disruptions*** in ***Saccharomyces*** ***cerevisiae***
AU Wach, Achim
CS Institut Angewandte Mikrobiologie, Universitaet Basel, Basel, CH-4056, Switz.
SO Yeast (1996), 12(3), 259-65 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB A PCR-method for fast prodn. of disruption cassettes is introduced, that allows the addn. of long flanking homol. regions of several hundred base pairs (LFH-PCR) to a marker module. Such a disruption cassette was made by linking two PCR fragments produced from genomic DNA to kanMX6, a modification of dominant resistance marker making S. ***cerevisiae*** resistant to geneticin (G418). In a first step, two several hundred base pairs long DNA fragments from the 5'- 3'-region of a S. ***cerevisiae*** gene were amplified in such a way that 26 base pairs extensions homologous to the kanMX6 marker were added to one of their ends. In a second step, one strand of each of these mols. then served as a long primer in a PCR using kanMX6 as template. When such a LFH-PCR-generated disruption cassette was used instead of a PCR-made disruption cassette flanked by short homol. regions, transformation efficiencies were increased by at least a factor of thirty. This modification will therefore also help to apply PCR-mediated gene manipulations to strains with decreased transformability and/or unpredictable sequence deviations.
OSC.G 443 THERE ARE 443 CAPLUS RECORDS THAT CITE THIS RECORD (443 CITINGS)

L11 ANSWER 69 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:142760 CAPLUS <<LOGINID::20110428>>
DN 124:222046
OREF 124:40905a,40908a
TI Selectable cassettes for simplified construction of ***yeast*** gene disruption vectors
AU Earley, Marie C.; Crouse, Gray F.

CS Graduate Program in Genetics and Molecular Biology, and Department of Biology, Emory University, Atlanta, GA, 30322, USA
SO Gene (1996), 169(1), 111-13 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier
DT Journal
LA English
AB Cassettes based on a hisG-URA3-hisG insert have been modified by the addn. of a KmR-encoding gene and flanking polylinker sites, greatly simplifying construction of gene disruption vectors in Escherichia coli. After ***gene*** ***disruption*** in ***yeast*** , URA3 can then be excised by recombination between the hisG repeats flanking the gene, permitting reuse of the URA3 ***marker*** .
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L11 ANSWER 70 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1996:104565 CAPLUS <<LOGINID::20110428>>
DN 124:166588
OREF 124:30703a,30706a
TI pMPY-ZAP: a reusable polymerase chain reaction-directed gene disruption cassette for ***Saccharomyces*** ***cerevisiae***
AU Schneider, B. L.; Steiner, B.; Seufert, W.; Futcher, A. B.
CS Cold Spring Harbor Lab., Cold Spring Harbor, NY, 11724, USA
SO Yeast (1996), 12(2), 129-34 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB Gene disruption is an important method for genetic anal. in ***Saccharomyces*** ***cerevisiae*** . We have designed a polymerase chain reaction-directed gene disruption cassette that allows rapid disruption of genes in S. ***cerevisiae*** without previously cloning them. In addn., this cassette allows recycling of URA3, generating ***gene*** ***disruptions*** without the permanent loss of the ura3 ***marker*** . An indefinite no. of disruptions can therefore by made in the same strain.
OSC.G 34 THERE ARE 34 CAPLUS RECORDS THAT CITE THIS RECORD (34 CITINGS)

L11 ANSWER 71 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:991306 CAPLUS <<LOGINID::20110428>>
DN 124:47514
OREF 124:8851a,8854a
TI Nature of abortive transformation in ***Saccharomyces*** ***cerevisiae***
AU Yap, Wendy Y.; Schiestl, Robert H.
CS Department Molecular Cellular Toxicology, Harvard School Public Health, Boston, MA, 02115, USA
SO Current Genetics (1995), 28(6), 517-20 CODEN: CUGED5; ISSN: 0172-8083
PB Springer
DT Journal
LA English
AB Disruption mutagenesis by homologous recombination in ***Saccharomyces*** ***cerevisiae*** is carried out by transforming-DNA fragments contg. the target ***gene*** ***disrupted*** by a selectable ***marker*** . A large no. of transient (abortive) transformants are often formed that may hinder the isolation of integrants contg. the gene disruption. The authors show that abortive transformants result from re-circularization of the linear transforming-DNA in vivo. Their no. was greatly reduced when the cut DNA could not readily re-ligate, either by digestions that gave non-compatible or blunt ends, or by de-phosphorylation. In addn., true integrants could be readily distinguished from abortive transformants through replica plating onto selective media. Enhanced disruption-mutagenesis was also obsd. when non-compatible ends were generated in an ARS-contg. insertion vector.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

L11 ANSWER 72 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:904331 CAPLUS <<LOGINID::20110428>>
DN 124:1743
OREF 124:395a,398a
TI Precise gene disruption in ***Saccharomyces*** ***cerevisiae*** by double fusion polymerase chain reaction
AU Amberg, David C.; Botstein, David; Beasley, Ellen M.
CS Dep. Genetics, Stanford Univ. School Medicine, Stanford, CA, 94305-5120, USA
SO Yeast (1995), 11(13), 1275-80 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB We adapted a fusion polymerase chain reaction (PCR) strategy to synthesize gene disruption alleles of any sequenced ***yeast*** gene of interest. The first step of the construction is to amplify sequences flanking the reading frame we want to disrupt and to amplify the selectable marker sequence. Then we fuse the upstream fragment to the marker sequence by fusion PCR, isolate this product and fuse it to the downstream sequence in a second fusion PCR reaction. The final PCR product can then be transformed directly into ***yeast*** . This method is rapid, relatively inexpensive, offers the freedom to choose from among a variety of selectable markers and allows one to construct precise disruptions of any sequenced open reading frame in ***Saccharomyces*** ***cerevisiae*** .
OSC.G 97 THERE ARE 97 CAPLUS RECORDS THAT CITE THIS RECORD (97 CITINGS)

L11 ANSWER 73 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:900757 CAPLUS <<LOGINID::20110428>>
DN 123:331757
OREF 123:59313a,59316a
TI The DNA and RNA polymerase genes of ***yeast*** plasmid pGKL2 are essential loci for plasmid integrity and maintenance
AU Schaffrath, Raffael; Soond, Surinder M.; Meacock, Peter A.
CS Department of Genetics, University of Leicester, Leicester, LE1 7RH, UK
SO Microbiology (Reading, United Kingdom) (1995), 141(10), 2591-9 CODEN: MROBEO; ISSN: 1350-0872
PB Society for General Microbiology
DT Journal
LA English
AB Novel recombinant plasmids derived from the Kluyveromyces lactis killer plasmid k2 have been constructed to study plasmid biol. and gene function. In vivo recombination between native resident k2 and suitable ***disruption*** vectors, employing the KITRP1 ***gene*** fused to a plasmid promoter as selection ***marker*** , yielded ORF2 and ORF6 deletion

plasmids at high frequencies. As judged from Southern hybridization and plasmid restriction mapping analyses, these novel hybrids, termed rd2/2 and rk2/6, resp., carry deletions in their putative DNA (ORF2) and RNA (ORF6) polymerase structural genes with central regions replaced by the input marker DNA. Long-term selection for TRP1 over 350 generations of growth did not favor maintenance of hybrids over wild-type k2. Thus, neither rk2/2 nor rk2/6 was fully functional and able to displace parental k2, indicating that both target genes are essential for plasmid integrity or maintenance. Recombinant plasmids were reduced in copy no. relative to k2 with rk2/2 more drastically affected than rk2/6 implying a direct involvement of the ORF2 product in plasmid replication and an indirect maintenance function for the ORF6 gene product.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)

L11 ANSWER 74 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:694648 CAPLUS <<LOGINID::20110428>>
DN 123:134215
OREF 123:23673a,23676a
TI Gene disruption with PCR products in ***Saccharomyces*** ***cerevisiae***
AU Lorenz, Michael C.; Muir, R. Scott; Lim, Eric; McElver, John; Weber, Shane C.; Heitmann, Joseph
CS Departments Genetics Pharmacology Howard Hughes Medical Inst., Duke Univ. Medical Cent., Durham, NC, 27710, USA
SO Gene (1995), 158(1), 113-17 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier
DT Journal
LA English
AB ***Gene*** ***disruption*** constructs were generated using PCR amplification of selectable ***markers*** with primers that provide homol. to the target gene of interest. Regions of homol. as short as 38-50 bp suffice to mediate homologous recombination in ***yeast*** . This technol. was applied to 3 specific ***yeast*** genes that would have been difficult to disrupt with current methods. By dispensing with the need to either clone the gene of interest or engineer a std. disruption construct, this method should facilitate anal. of sequenced genes of unknown function, which will soon include the entire ***yeast*** genome.
OSC.G 193 THERE ARE 193 CAPLUS RECORDS THAT CITE THIS RECORD (193 CITINGS)

L11 ANSWER 75 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:563098 CAPLUS <<LOGINID::20110428>>
DN 123:189560
OREF 123:33505a,33508a
TI Isolation of Schizosaccharomyces pombe isopentenyl diphosphate isomerase cDNA clones by complementation and synthesis of the enzyme in Escherichia coli
AU Hahn, Frederick M.; Poulter, C. Dale
CS Dep. Chem., Univ. Utah, Salt Lake City, UT, 84112, USA
SO Journal of Biological Chemistry (1995), 270(19), 11298-303 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Isopentenyl diphosphate (IPP) isomerase catalyzes an essential activation step in the isoprene biosynthetic pathway. The ***Saccharomyces*** ***cerevisiae*** gene for IPP isomerase, IDI1, was recently isolated and characterized, and the wild-type ***gene*** , IDI1, was ***disrupted*** with a LEU2 ***marker*** to create a diploid ***yeast*** stain heterozygous for the idi1::Leu2 ***disruption*** , which revealed that IDI1 was an essential single-copy ***gene*** . A cDNA clone from Schizosaccharomyces pombe was now isolated by a plasmid shuffle-mediated complementation of the LEU2-disrupted ***yeast*** gene. The S. pombe cloned encoded a 26,864-Da polypeptide of 227 amino acids with a high degree of similarity to the S. ***cerevisiae*** IDI1 enzyme. S. pombe IPP isomerase contained the essential Cys and Glu catalytic residues identified in ***yeast*** isomerase but was significantly smaller than the S. ***cerevisiae*** enzyme. The plasmid shuffle tech. is an excellent procedure for screening expression libraries for IPP isomerase activity by complementation of the idi1 mutation.
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)

L11 ANSWER 76 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:497010 CAPLUS <<LOGINID::20110428>>
DN 122:283348
OREF 122:51486h,51487a
TI Strategy for deletion of complete open reading frames in ***Saccharomyces*** ***cerevisiae***
AU Eberhardt, Ines; Hohmann, Stefan
CS Laboratorium voor Moleculaire Celbiologie, Katholieke Universiteit te Leuven, Flanders, Belg.
SO Current Genetics (1995), 27(4), 306-8 CODEN: CUGED5; ISSN: 0172-8083
PB Springer
DT Journal
LA English
AB The classical disruption method for ***yeast*** genes is by using in vitro deletion of the gene of interest, or of a part of it, with restriction enzymes. We are now routinely using a strategy that takes advantage of polymerase chain reactions (PCRs) which amplify large pieces of DNA. Since this approach results in a complete, precise deletion of the open reading frame, which is replaced by a unique restriction site, the ligated PCR can be used for the insertion of different ***markers*** or for two-step ***gene*** ***disruptions*** without an inserted ***marker*** . As we have now used this strategy for the deletion of more than ten genes we have in this report included some hints based on our experience.
OSC.G 27 THERE ARE 27 CAPLUS RECORDS THAT CITE THIS RECORD (27 CITINGS)

L11 ANSWER 77 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:497008 CAPLUS <<LOGINID::20110428>>
DN 122:283414
OREF 122:51499a,51502a
TI Construction of a ***marker*** ***gene*** cassette which is repeatedly usable for ***gene*** ***disruption*** in ***yeast***
AU Toh-e, Akio
CS Faculty Science, Univ. Tokyo, Tokyo, 113, Japan
SO Current Genetics (1995), 27(4), 293-7 CODEN: CUGED5; ISSN: 0172-8083
PB Springer
DT Journal
LA English
AB A disruption cassette has been constructed contg. the LEU2 gene flanked by directly repeated site-specific recombination sites of the ***yeast*** plasmid, pSB3, which resembles the 2

.mu.m DNA of ***Saccharomyces*** ***cerevisiae*** . A disruption constructed by inserting this DNA fragment acquires a Leu+ phenotype, which can be easily removed by expressing the FLP-PSB3 gene encoding the site-specific recombinase of pSB3. A test was made using a Schizosaccharomyces pombe host. The ura4+ gene of S. pombe was replaced with the ura4::LEU2 gene constructed by inserting the disruption cassette into the ura4+ gene. Then, the FLP-pSB3 gene driven by the nmt1+ promoter was introduced into this disruptant. Upon de-repression of the nmtI promoter by removing thiamine from the medium, the rate of appearance of Leu- was increased. As expected the ura4+ locus underwent a structural change. Thus, the FLP-pSB3 protein and its target site can function adequately in S. pombe.
OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)

L11 ANSWER 78 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:485010 CAPLUS <<LOGINID::20110428>>
DN 123:2045
OREF 123:467a,470a
TI A novel method employing polymerase chain reaction to disrupt genes lacking convenient restriction enzyme sites in ***yeast***
AU Wu, Mian; Shang, Hui-Shen; Yeong, Ching-Yuen; Tan, Priscilla Hui-Ning; Lu, Zhen-Xin; Wong, Sek-Man
CS Institute of Molecular and Cell Biology, National University of Singapore, Singapore, 0511, Singapore
SO Molecular Biotechnology (1995), 3(1), 72-4 CODEN: MLBOEO; ISSN: 1073-6085
DT Journal
LA English
AB A novel method employing polymerase chain reaction was developed for the disruption of ***yeast*** genes lacking convenient restriction enzyme sites. The method was found to be easy and effective. Using this method, a ***yeast*** YKE2 gene (a ***yeast*** homolog of murine k-region expressed ***genes***) was successfully ***disrupted*** by replacement of HIS3 ***marker*** ***gene*** .

L11 ANSWER 79 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:466958 CAPLUS <<LOGINID::20110428>>
DN 123:75819
OREF 123:13287a,13290a
TI New heterologous modules for classical or PCR-based gene disruptions in ***Saccharomyces*** ***cerevisiae***
AU Wach, Achim; Brachat, Arndt; Pohlmann, Rainer; Philippsen, Peter
CS Inst. Angewandte Mikrobiol., Univ. Basel, Basel, CH-4056, Switz.
SO Yeast (1994), 10(13), 1793-808 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB We have constructed and tested a dominant resistance module, for selection of S. ***cerevisiae*** transformants, which entirely consists of heterologous DNA. This kanMX module contains the known kanr open reading-frame of the E. coli transposon Tn903 fused to transcriptional and translational control sequences of the TEF gene of the filamentous fungus Ashbya gossypii. This hybrid module permits efficient selection of transformants resistant against geneticin (G418). We also constructed a lacZMT reporter module in which the open reading-frame of the E. coli lacZ gene (lacking the first 9 codons) is fused at its 3' end to the s. ***cerevisiae*** ADH1 terminator. KanMX and the lacZMT module, or both modules together, were cloned in the center of a new multiple cloning sequence comprising 18 unique restriction sites flanked by Not I sites. Using the double module for constructions of in-frame substitutions of genes, only one transformation expt. is necessary to test the activity of the promoter and 10 search for phenotypes due to inactivation of this gene. To allow for repeated use of the G418 selection some kanMX modules are flanked by 470 bp direct repeats, promoting in vivo excision with frequencies of 10-3-10-4. The 1.4 kb kanMX module was also shown to be very useful for PCR based gene disruptions. In an expt. in which a gene disruption was done with DNA mols. carrying PCR-added terminal sequences of only 35 bases homol. to each target site, all twelve tested geneticin-resistant colonies carried the correctly integrated kanMX module.
OSC.G 1562 THERE ARE 1562 CAPLUS RECORDS THAT CITE THIS RECORD (1563 CITINGS)

L11 ANSWER 80 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:444473 CAPLUS <<LOGINID::20110428>>
DN 123:189961
OREF 123:33589a,33592a
TI Phosphatidylserine decarboxylase 2 of ***Saccharomyces*** ***cerevisiae*** . Cloning and mapping of the gene, heterologous expression, and creation of the null allele
AU Trotter, Pamela J.; Pedretti, John; Yates, Rachel; Voelker, Dennis R.
CS Natl. Jewish Cent. Immunol. Respiratory Med., Denver, CO, 80206, USA
SO Journal of Biological Chemistry (1995), 270(11), 6071-80 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The ***yeast*** ***Saccharomyces*** ***cerevisiae*** expresses two phosphatidylserine decarboxylase (PSD) activities which are responsible for conversion of phosphatidylserine to phosphatidylethanolamine, and either enzyme alone is sufficient for normal cellular growth. However, strains contg. a PSD1 null allele and a mutation leading to loss of PSD2 activity (psd1-.DELTA.1::TRP1 psd2) are auxotrophic for ethanolamine. This nutritional requirement was utilized to isolate the gene encoding the PSD2 enzyme by complementation. The PSD2 gene encodes a protein of 1138 amino acids with a predicted mol. mass of 130 kDa. The deduced amino acid sequence shows significant identity (34%) to a PSD-like sequence from Clostridium pasteurianum and the ***yeast*** PSD1 (19%) at the carboxyl end of the protein. Of particular interest is the presence of a sequence, GGST, which may be involved in post-translational processing and prosthetic group formation similar to other PSD enzymes. The PSD2 amino acid sequence also shows significant homol. to the C2 regions of protein kinase C and synaptotagmin. Phys. mapping expts. demonstrate that the PSD2 is located on chromosome 7. The PSD2 gene was heterologously expressed by infection of Sf-9 insect cells with recombinant baculovirus, resulting in a 10-fold increase in PSD activity. The null allele of PSD2 was introduced into ***yeast*** strains by one-step ***gene*** deletion/ ***disruption*** with a HIS3 ***marker*** ***gene*** . Strains expressing wild type PSD1 and the psd2-.DELTA.1:: HIS3 allele show a small decrease in overall PSD activity, but no noticeable effect upon [3H]serine incorporation into aminophospholipids. Strains contg. both the psd1-

.DELTA.1::TRP1 and psd2-.DELTA.1::HIS3 null alleles, however, express no detectable PSD activity, are ethanolamine auxotrophs and show a severe deficit in the conversion of [3H]serine-labeled phosphatidylserine to phosphatidylethanolamine. These data indicate that the gene isolated is the structural gene for PSD2 and that the PSD1 and PSD2 enzymes account for all ***yeast*** PSD activity.
OSC.G 88 THERE ARE 88 CAPLUS RECORDS THAT CITE THIS RECORD (88 CITINGS)

L11 ANSWER 81 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:361281 CAPLUS <<LOGINID::20110428>>
DN 122:307757
OREF 122:55825a,55828a
TI Molecular cloning of the plc1+ gene of Schizosaccharomyces pombe, which encodes a putative phosphoinositide-specific phospholipase C
AU Andoh, Tomoko; Yoko-O, Takehiko; Matsui, Yasushi; Toh-E, Akio
CS Grad. Sch. Sci., Univ. Tokyo, Tokyo, 113, Japan
SO Yeast (1995), 11(2), 179-85 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB Exploiting the polymerase chain reaction, the authors have isolated a gene that endoes a putative phosphoinositide-specific phospholipase C (PLC) of the fission ***yeast*** S. pombe. Inspection of the nucleotide sequence of the gene revealed an open reading frame that can encode a polypeptide of 899 amino acid residues with a calcd. mol. mass of 102 kDa. This putative polypeptide contains both the X and Y regions that are conserved among 3 classes of mammalian PLC, and also contains a presumptive Ca2+-binding site (an E-F hand motif). The structure of the putative protein is most similar to that of the .delta. class of PLC isoenzymes. To investigate the role of this structure of the putative protein is most similar to that of the .delta. class of PLC isoenzymes. To investigate the role of this ***gene*** , designated plc1+, ***gene*** ***disruption*** was carried out by ***interrupting*** the coding region with the ura4+ ***marker*** . Growth of plc1 cells was temp.-sensitive in rich medium, and cells could not grow in synthetic medium. Expression of the PLC1 gene of ***Saccharomyces*** ***cerevisiae*** suppressed the growth defect phenotype of plc1- cells, a strong suggestion that the plc1+ gene encodes PLC. The PLC1 sequence appears in the public data libraries, DDBJ GenBank, EMBL under the following Accession No.: D38309.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)

L11 ANSWER 82 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:224941 CAPLUS <<LOGINID::20110428>>
DN 122:24853
OREF 122:4793a,4796a
TI A family of vectors that facilitate transposon and insertional mutagenesis of cloned genes in ***yeast***
AU Allen, James B.; Elledge, Stephen J.
CS Verna & Marrs McLean Dep. Biochemistry, Howard Hughes Medical Institute, Houston, TX, 77030, USA
SO Yeast (1994), 10(10), 1267-72 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB This report describes two sets of plasmid vectors that facilitate the identification of regions of complementation in cloned genomic inserts via transposon or insertional mutagenesis. The first set contains ARS-H4 CEN6, a ***yeast*** selectable nutritional marker (HIS3, TRP1 or URA3), and neo for selection in Escherichia coli. These plamids lack the Tn3 transposition immunity region present in pBR322 derived vectors, and are permissive recipients for Tn3 transposon mutagenesis. The second family of plasmids described facilitate gene disruption procedures performed in vitro. These vectors carry disruption cassettes that contain different ***yeast*** selectable markers (HIS3, LEU2, TRP1 or URA3) adjacent to the Tn5 neo gene. These genes can be excised as a cassette on a common restriction fragment and introduced into any desired restriction site with selection for kanamycin resistance.
OSC.G 23 THERE ARE 23 CAPLUS RECORDS THAT CITE THIS RECORD (23 CITINGS)

L11 ANSWER 83 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1995:20973 CAPLUS <<LOGINID::20110428>>
DN 122:24744
OREF 122:4773a,4776a
TI Locating, DNA sequencing, and disrupting ***yeast*** genes using tagged Tn1000
AU Sedgwick, Steven G.; Morgan, Brian A.
CS Lab. Yeast Genet., Natl. Inst. Med. Res., London, NW7 1AA, UK
SO Methods in Molecular Genetics (1994), 3(MOLECULAR MICROBIOLOGY TECHNIQUES, PT. A), 131-40 CODEN: MEMGE6; ISSN: 1067-2389
DT Journal
LA English
AB The aim of this chapter is to describe and encourage the use of simple methods of Tn1000 transposition mutagenesis to study cloned genes from ***Saccharomyces*** ***cerevisiae*** . Tn1000 derivs. are described which carry S. ***cerevisiae*** ***markers*** that can be used for selecting ***disruptions*** of ***yeast*** chromosomal ***genes*** .
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)

L11 ANSWER 84 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1994:673140 CAPLUS <<LOGINID::20110428>>
DN 121:273140
OREF 121:49667a,49670a
TI Recycling selectable markers in ***yeast***
AU Sauer, Brian
CS DuPont Merck Pharm. Co., Wilmington, DE, USA
SO BioTechniques (1994), 16(6), 1086-8 CODEN: BTNQDO; ISSN: 0736-6205
DT Journal
LA English
AB A series of excisable marker cassettes has been constructed to facilitate recycling of selectable markers in ***yeast*** . These cassettes exploit the use of the Cre DNA recombinase to precisely excise the marker gene when desired. They are esp. useful for making ***gene*** ***disruptions*** and then removing the ***marker*** ***gene*** to allow subsequent genetic manipulations with that same ***marker*** . Also described are a no. of cre expression vectors that allow galactose-induced expression of the

recombinase in ***yeast*** . The procedure is simple and allows rapid processing of large nos. of transformants.
OSC.G 25 THERE ARE 25 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

L11 ANSWER 85 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1994:450964 CAPLUS <<LOGINID::20110428>>
DN 121:50964
OREF 121:9035a,9038a
TI Cloning and sequencing of the ura3 locus of the methylotrophic ***yeast*** Hansenula polymorpha and its use for the generation of a deletion by gene replacement
AU Merckelbach, Armin; Goedecke, Stefanie; Janowicz, Zgigniew A.; Hollenberg, Cornelis P.
CS Rhein Biotech GmbH, Duesseldorf, D-40595, Germany
SO Applied Microbiology and Biotechnology (1993), 40(2-3), 361-4 CODEN: AMBIDG; ISSN: 0175-7598
DT Journal
LA English
AB The ura3 gene on Hansenula polymorpha was cloned, sequenced and used to generate a ura3 mutant from the wild-type strain of this ***yeast*** via integrative mutagenesis. The Tn5 neomycin-resistance marker (neo) under control of the ADH1 promoter from ***Saccharomyces*** ***cerevisiae*** served as a transformation marker. The results show that gene replacement can be achieved in H. polymorpha, a ***yeast*** with a high level of non-homologous integration.
OSC.G 35 THERE ARE 35 CAPLUS RECORDS THAT CITE THIS RECORD (35 CITINGS)

L11 ANSWER 86 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1994:316857 CAPLUS <<LOGINID::20110428>>
DN 120:316857
OREF 120:55525a,55528a
TI Generation of random internal deletion derivatives of YACs by homologs targeting to Alu sequences
AU Soh, Jaemog; Mariano, Thomas M.; Bradshaw, Gary; Donnelly, Robert J.; Pestka, Sidney
CS Robert Wood Johnson Med. Sch., Univ. Med. and Dent. New Jersey, Piscataway, NJ, 08854-5635, USA
SO DNA and Cell Biology (1994), 13(3), 301-9 CODEN: DCEBE8; ISSN: 1044-5498
DT Journal
LA English
AB To facilitate the manipulation of human genomic DNA in ***yeast*** artificial chromosome (YAC) clones, a plasmid to integrate the selective marker for antibiotic G418 resistance into YACs and to delete some of the human DNA fragments from YACs was constructed. The linearized integration/deletion plasmid, which contains Alu family sequences at both ends, can recombine with YACs contg. human repetitive sequences via homologous recombination. The homologous recombination results in a random integration of the antibiotic G418-resistant gene into a human genomic Alu sequence, and in most cases, an internal deletion within the YAC. The YACs with internal deletions can be useful to identify the location of the genes if they produce functional knockouts. In those cases when the integration/deletion event ***disrupts*** the integrity of the ***gene*** so it no longer can produce a viable and functional mRNA in fused eukaryotic cells, the site of integration in the YAC thus serves as a ***marker*** for the inactivated gene. In this report the authors described a model system to locate specific genes in YACs.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L11 ANSWER 87 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1994:126377 CAPLUS <<LOGINID::20110428>>
DN 120:126377
OREF 120:22121a,22124a
TI A ***Saccharomyces*** ***cerevisiae*** homolog of mammalian translation factor 4B contributes to RNA helicase activity
AU Altmann, Michael; Mueller, Peter P.; Wittmer, Barbara; Ruchti, Franziska; Lanker, Stefan; Trachsel, Hans
CS Inst. Biochem. Mol. Biol., Univ. Berne, Bern, 3012, Switz.
SO EMBO Journal (1993), 12(10), 3997-4003 CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB The TIF3 gene of ***Saccharomyces*** ***cerevisiae*** was cloned and sequenced. The deduced amino acid sequence shows 26% identity with the sequence of mammalian translation initiation factor eIF-4B. The TIF3 gene is not essential for growth; however, its disruption results in a slow growth and cold-sensitive phenotype. In vitro translation of total ***yeast*** RNA in an ext. from a TIF3 gene-disrupted strain is reduced compared with a wild-type ext. The translational defect is more pronounced at lower temps. and can be cor. by the addn. of wild-type ext. or mammalian eIF-4B, but not by addn. of mutant ext. In vivo translation of .beta.-galactosidase ***reporter*** mRNA with varying degree of RNA secondary structure in the 5' leader region in a TIF3 ***gene*** - ***disrupted*** strain shows preferential inhibition of translation of mRNA with more stable secondary structure. This indicates that Tif3 protein is an RNA helicase or contributes to RNA helicase activity in vivo.
OSC.G 62 THERE ARE 62 CAPLUS RECORDS THAT CITE THIS RECORD (62 CITINGS)

L11 ANSWER 88 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1994:70417 CAPLUS <<LOGINID::20110428>>
DN 120:70417
OREF 120:12547a,12550a
TI Cloning and manipulation of the Schizosaccharomyces pombe his7+ gene as a new selectable marker for molecular genetic studies
AU Apolinario, Ethel; Nocero, Mary; Jin, Mei; Hoffman, Charles S.
CS Dep. Biol., Boston Coll., Chestnut Hill, MA, 02167, USA
SO Current Genetics (1993), 24(6), 491-5 CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB The authors have cloned the his7+ gene of the fission ***yeast*** Schizosaccharomyces pombe by complementation of the recessive mutant allele his7-366. The his7+ gene is able to complement a mutation of the Escherichia coli hisI gene, suggesting that his7+ encodes a phosphoribosyl-AMP cyclohydrase. Subcloning expts. localize the gene to a 1.9-kb XbaI-BglII fragment. The authors describe the construction of plasmids to facilitate the use of his7+ as a selectable marker in S. pombe studies. Plasmid pEA2 carries his7+ cloned into the pUC18 polylinker. From either pEA2 or the original his7+ clone, pMN2, fragments carrying his7+ can be isolated using a variety of restriction enzymes for the construction of gene disruptions. Plasmid pEA500 is a cloning vector that carries his7+ and ars1,

yet retains the ability to use the blue/white color screen to identify recombinants.
OSC.G 41 THERE ARE 41 CAPLUS RECORDS THAT CITE THIS RECORD (41 CITINGS)

L11 ANSWER 89 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1994:24498 CAPLUS <<LOGINID::20110428>>
DN 120:24498
OREF 120:4481a,4484a
TI An "in-out" strategy using gene targeting and FLP recombinase for the functional dissection of complex DNA regulatory elements: Analysis of the .beta.-globin locus control region
AU Fiering, Steven; Kim, Chul G.; Epner, Elliot M.; Groudine, Mark
CS Fred Hutchinson Cancer Res. Cent., Seattle, WA, 98104, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1993), 90(18), 8469-73 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The human .beta.-globin locus control region (LCR) is a complex DNA regulatory element that controls the expression of the cis-linked .beta.-like globin genes located in the 55 kilobases 3' of the LCR. The authors have initiated the functional anal. of the LCR by homologous recombination in murine erythroleukemia cell somatic hybrids that carry a single copy of human chromosome 11 on which the .beta.-globin locus is situated. High-level expression of the human .beta.-globin gene normally occurs when these hybrid cells are induced to differentiate. The authors have reported that the insertion of an expressed selectable ***marker*** ***gene*** (driven by the Friend virus enhancer/promoter) into the LCR ***disrupts*** the LCR-mediated regulation of globin transcription. In these cells, .beta.-globin is no longer expressed when the cells differentiate; instead, expression of the selectable marker gene increases significantly after differentiation. Since present techniques for homologous recombination require the insertion of a selectable marker, further progress in using homologous recombination to analyze the LCR depends on deletion of the selectable marker and demonstration that the locus functions normally after the insertion, expression, and deletion of the selectable marker. Here the authors show that after precise deletion of the selectable marker by using the FLP recombinase/FRT (FLP recombinase target) system, the locus functions as it did before the homologous recombination event. These studies demonstrate the feasibility of using homologous recombination to analyze the LCR in particular, and other complex cis-regulatory DNA elements in general, in their normal chromosomal context.
OSC.G 69 THERE ARE 69 CAPLUS RECORDS THAT CITE THIS RECORD (69 CITINGS)

L11 ANSWER 90 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1993:510271 CAPLUS <<LOGINID::20110428>>
DN 119:110271
OREF 119:19677a,19680a
TI Heterologous gene expression with ***yeast*** linear plasmids
AU Meinhardt, F.; Schaffrath, R.; Schruender, J.
CS Inst. Mikrobiol., Westfael. Wilhelms-Univ. Muenster, Munester, W-4400, Germany
SO Mededelingen van de Faculteit Landbouwwetenschappen, Universiteit Gent (1992), 57(4b), 2071-6 CODEN: MFLRA3; ISSN: 0368-9697
DT Journal
LA English
AB A discussion is given on linear DNA plasmids pGKL1 and pGKL2 of Kluyveromyces lactis that are assocd. with the killer phenotype. Construction of the linear plasmids by in vivo recombination, integration of detectable ***marker*** genes into a locus of a linear plasmid, ***gene*** expression and organization, and the application of a ***gene*** ***disruption*** system for cytoplasmically localized killer plasmids are discussed.

L11 ANSWER 91 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1993:464390 CAPLUS <<LOGINID::20110428>>
DN 119:64390
OREF 119:11433a,11436a
TI Characterization of cspB, a Bacillus subtilis inducible cold shock gene affecting cell viability at low temperatures
AU Willimsky, Gerald; Bang, Holger; Fischer, Gunter; Marahiel, Mohamed A.
CS Fachbereich Chem. Biochem., Philipps-Univ. Marburg, Marburg, W-3550, Germany
SO Journal of Bacteriology (1992), 174(20), 6326-35 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB A new class of cold shock-induced proteins that may be involved in an adaptive process required for cell viability at low temps. or may function as antifreeze proteins in Escherichia coli and ***Saccharomyces*** ***cerevisiae*** has been identified. A small B. subtilis cold shock protein (CspB) was purified and its amino-terminal sequence was detd. By using mixed degenerate oligonucleotides, the corresponding gene (cspB) was cloned on two overlapping fragments of 5 and 6 kb. The gene encodes an acidic 67 amino-acid protein (pI 4.31) with a predicted mol. mass of 7365 Da. Nucleotide and deduced amino acid sequence comparisons revealed 61% identity to the major cold shock protein of E. coli and 43% identity to a family of eukaryotic DNA binding proteins. Northern RNA blot and primer extension studies indicated the presence of one cspB transcript that was initiated 119 bp upstream of the initiation codon and was found to be induced severalfold when exponentially growing B. subtilis cell cultures were transferred from 37.degree. to 10.degree.. Consistent with this cold shock induction of cspB mRNA, a six- to eight-fold induction of cspB-directed .beta.-galactosidase synthesis was obsd. upon downshift in temp. To investigate the function of CspB, the cold shock protein was inactivated by replacing the cspB ***gene*** in the B. subtilis chromosome with a cat- ***interrupted*** copy (cspB::cat) by ***marker*** replacement recombination. The viability of cells of this mutant strain, GW1, at freezing temps. was strongly affected. However, the effect of having no CspB in GW1 could be slightly compensated for when cells were preincubated at 10.degree. before freezing. These results indicate that CspB belongs to a new type of stress-inducible proteins that might be able to protect B. subtilis cells from damage caused by ice crystal formation during freezing.
OSC.G 114 THERE ARE 114 CAPLUS RECORDS THAT CITE THIS RECORD (114 CITINGS)

L11 ANSWER 92 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1993:442018 CAPLUS <<LOGINID::20110428>>
DN 119:42018
OREF 119:7495a

TI Directed mutagenesis in an asporogenous methylotrophic ***yeast*** : cloning, sequencing, and one-step ***gene*** ***disruption*** of the 3-isopropylmalate dehydrogenase ***gene*** (LEU2) of Candida boidinii to derive doubly auxotrophic ***marker*** strains
AU Sakai, Yasuyoshi; Tani, Yoshiki
CS Fac. Agric., Kyoto Univ., Kyoto, 606-01, Japan
SO Journal of Bacteriology (1992), 174(18), 5988-93 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB A model system for one-step gene disruption for an asporogenous methylotrophic ***yeast*** , Candida boidinii, is described. In this system, the 3-isopropylmalate dehydrognase gene (C. boidinii LEU2) was selected as the target gene for disruption to derive new host strains for transformation. First, the C. biodinii LEU2 gene was cloned, and its complete nucleotide sequence was detd. Next, the LEU2 ***disruption*** vectors, which had the C. boidinii URA3 ***gene*** as the selectable ***marker*** , were constructed. Of the Ura+ transformants obtained with these plasmids, more than half showed a Leu- phenotype. Finally, the double-marker strains of C. boidinii were derived. When vectors with repeated flanking sequences of the C. boidinii URA3 gene were used for gene disruption, Leu- Ura+ transformants changed spontaneously to a Leu- Ura- phenotype .apprx.100 times more frequently than they did when plasmids without the repeated sequences were used. Southern anal. showed that these events included a one-step gene disruption and a subsequent popping out of the C. boidinii URA3 sequence from the transformant chromosome.
OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (28 CITINGS)

L11 ANSWER 93 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1993:402053 CAPLUS <<LOGINID::20110428>>
DN 119:2053
OREF 119:435a,438a
TI SEC6 encodes an 85 kDa soluble protein required for exocytosis in ***yeast***
AU Potenza, Marc; Bowser, Robert; Muller, Heike; Novick, Peter
CS Sch. Med., Yale Univ., New Haven, CT, 06510, USA
SO Yeast (1992), 8(7), 549-58 CODEN: YESTE3; ISSN: 0749-503X
DT Journal
LA English
AB The SEC6 gene encodes a protein required for an event leading to fusion of post-Golgi vesicles with the plasma membrane in ***Saccharomyces*** ***cerevisiae*** cells. The gene was cloned by complementation of the temp.-sensitive growth defect of a sec6-4 strain. The nucleotide sequence was detd. and the longest open reading frame was found to encode an 85 kDa protein of 733 amino acids. The Sec6 protein is predicted to be hydrophilic and is found predominantly in the sol. fraction of a ***yeast*** lysate, in a species that sediments with a coeff. of 14 S. No extensive homol. was found with known proteins of the database. ***Gene*** ***disruption*** and ***marker*** rescue expts. indicate that SEC6 is a single copy gene essential for growth. Overprodn. of Sec6p does not suppress any of the other late-acting sec mutants, yet sec6-4 does display synthetic lethality with sec8-9, suggesting that the 2 gene products may fulfill inter-related functions.
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)

L11 ANSWER 94 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1993:248764 CAPLUS <<LOGINID::20110428>>
DN 118:248764
OREF 118:42987a,42990a
TI Cloning and sequence analysis of a Candida maltosa gene which confers resistance to cycloheximide
AU Sasnauskas, K.; Jomantiene, R.; Lebediene, E.; Lebedys, J.; Januska, A.; Janulaitis, A.
CS Dep. Mol. Biol., Inst. Appl. Enzymol., Vilnius, 2028, Lithuania
SO Gene (1992), 116(1), 105-8 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB A CYHR gene from C. maltosa, which confers resistance to cycloheximide, was cloned in ***Saccharomyces*** ***cerevisiae*** . A 2.3-kb DNA fragment carrying this gene was sequenced, and an open reading frame able to encode 553 amino acids (aa) was found in the sequence. Computer searches of the GenBank, EMBL, SWIS-PROT and Gen-Pept databases using the FASTA program failed to detect any proteins with extensive similarities to the deduced aa sequence for CYHR. The cloned gene transforms S. ***cerevisiae*** at a frequency similar to auxotrophic ***markers*** and can be used as a dominant selectable ***marker*** for introducing recombinant plasmids into wild-type strains of S. ***cerevisiae*** , as well as for ***gene*** ***disruption*** expts.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

L11 ANSWER 95 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1993:226916 CAPLUS <<LOGINID::20110428>>
DN 118:226916
OREF 118:39039a,39042a
TI Genes for directing vacuolar morphogenesis in ***Saccharomyces*** ***cerevisiae*** . II. VAM7, a gene for regulating morphogenic assembly of the vacuoles
AU Wada, Yoh; Anraku, Yasuhiro
CS Fac. Sci., Univ. Tokyo, Tokyo, 113, Japan
SO Journal of Biological Chemistry (1992), 267(26), 18671-5 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB VAM7 Gene function has been shown to be required for proper morphogenesis of the vacuole in ***yeast*** . The DNA fragments that complemented the defective vacuolar morphol. of the vam7-1 mutation were isolated from a ***yeast*** genomic library. An overlapping 2.5-kilobase BglII-HindIII region was found to be sufficient for complementation of the vam7-1 phenotype. This fragment was integrated at the chromosomal VAM7 locus, indicating that it contained an authentic VAM7 gene. On nucleotide sequencing of the VAM7 gene, an open reading frame of 948 base pairs, coding for a hydrophilic polypeptide of 316 amino acid residues, was identified. The deduced amino acid sequence of the carboxyl-terminal region of the VAM7 gene product has heptad repeats and shows the potential ability to form a coiled-coil structure. ***Disruption*** of VAM7 was not lethal; cells with a ***disrupted*** VAM7 ***gene*** did not, however, have prominent large vacuoles but rather numerous small compartments that accumulated the histochem. ***marker*** mol. of the vacuolar compartment. They contained mature forms of the vacuolar marker proteins carboxypeptidase Y and vacuolar glycoprotein vgp72. A mutant with both vam7 and vam5 null

mutations was constructed and shown to have neither vacuolar structures stained with ade-related fluorochrome nor mature forms of vacuolar marker proteins. These findings suggested that the VAM7 gene product functions in the process of morphogenic assembly of the vacuolar compartment but is not involved in protein sorting and delivery to the vacuole.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)

L11 ANSWER 96 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1993:141092 CAPLUS <<LOGINID::20110428>>
DN 118:141092
OREF 118:24139a,24142a
TI A role for reverse transcripts in gene conversion
AU Derr, Leslie K.; Strathern, Jeffrey N.
CS Frederick Cancer Res. Dev. Cent., NCI, Frederick, MD, 21702, USA
SO Nature (London, United Kingdom) (1993), 361(6408), 170-3 CODEN: NATUAS; ISSN: 0028-0836
DT Journal
LA English
AB Recombination between a reverse transcript and its chromosomal homolog was demonstrated using an assay that specifically detects this recombination pathway in ***Saccharomyces*** ***cerevisiae*** . A plasmid contg. a his3 ***reporter*** ***gene*** ***interrupted*** by an artificial intron in an unspliceable orientation to the HIS3 promoter was prepd. However, a GAL1 promoter at the 3' end of the his3 gene produces a spliceable transcript. DNA recombination between a reverse transcript of this his3 antisense RNA and a his3 deletion mutation introduced into the MAT locus on chromosome III resulted in His3+ prototrophy.
OSC.G 53 THERE ARE 53 CAPLUS RECORDS THAT CITE THIS RECORD (53 CITINGS)

L11 ANSWER 97 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1993:33661 CAPLUS <<LOGINID::20110428>>
DN 118:33661
OREF 118:6026h,6027a
TI An easy and fast alternative to plasmid shuffling for the identification of in vitro mutagenized alleles of essential genes of ***Saccharomyces*** ***cerevisiae***
AU Froehlich, Kai Uwe; Ruediger, Manfred; Eberhardt, Dorit; Mecke, Dieter
CS Physiol. Chem. Inst., Tuebingen, 7400, Germany
SO Nucleic Acids Research (1992), 20(22), 6113-14 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB An improved strategy similar to plasmid shuffling was developed which avoids its disadvantages, uses fewer steps, and requires the construction of one plasmid only. Meiosis instead of plasmid loss is employed to sep. the wild type gene from the mutant allele. The strategy also begins with ***disrupting*** the desired ***gene*** in a diploid strain, replacing it with a ***marker*** gene. This strain is then transformed with the mutagenized plasmid. The strain is brought to sporulation; mass spores are isolated and plated on a medium selecting for the disrupting marker. Alternatively, the spores can be plated on complex media, and the segregant colonies can then be replica plated for selection, to avoid the loss of mutants unable to germinate on minimal media. The strategy allows for easy isolation of a great no. of potential mutants, because they do not have to be picked manually previous to selection for loss of the wild type gene. The segregants grow as singular colonies without a background lawn of undesired cells, easing detection of mutants with marginal growth. Using meiosis as the means for allele sepn. also avoids phases of growth where cells contg. undamaged forms of the gene of interest proliferate faster than those with a damaged gene and thereby increase their proportion in the mixt. Because of their wild type copy of the gene, all diploids should sporulate at the same rate. Therefore, all transformants are represented in the spore suspension in equal portions.

L11 ANSWER 98 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1992:606027 CAPLUS <<LOGINID::20110428>>
DN 117:206027
OREF 117:35413a,35416a
TI A hit-and-run system for targeted genetic manipulations in ***yeast***
AU Roca, Joaquim; Gartenberg, Marc R.; Oshima, Yasuji; Wang, James C.
CS Dep. Biochem., Harvard Univ., Cambridge, MA, 02138, USA
SO Nucleic Acids Research (1992), 20(17), 4671-2 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB One of the most powerful techniques in the manipulation of ***yeast*** genes is the one-step gene transplacement method: a selectable genetic marker, flanked by sequences A and B that are homologous to their corresponding sequences in the target, is used to replace the region between A and B of the target through homologous recombination. In multiple transplacements or in cases when several genetically marked plasmids are to be used to transform the resulting mutants, however, there is often a shortage of selectable markers. A hit-and-run system based on a site-specific recombinase from the ***yeast*** Zygosaccharomyces rouxii was used for gene transplacement in ***Saccharomyces*** ***cerevisiae*** . In this method, the selectable genetic ***marker*** for ***gene*** - ***disruption*** is flanked by two 58 base pair direct repeats that are the recombination sites of the Z. rouxii enzyme; induction of the recombinase following ***gene*** - ***disruption*** excises the ***marker*** . Plasmid pJR-URA3 contains a URA3 cassette. For a particular gene transplacement, the cassette is cloned in between the desired sequences for homologous recombination. The one-step gene transplacement procedure is then performed with a S. ***cerevisiae*** strain by sequential or simultaneous transformation with a linear DNA contg. the URA3 cassette and pHM53, which carries a LEU2 marker and the Z. rouxii recombinase gene expressed from the glucose-repressible and galactose-inducible promoter of the S. ***cerevisiae*** GAL1 gene. The system was demonstrated with the transplacement of gene TOP1 of S. ***cerevisiae*** .
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

L11 ANSWER 99 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1992:505380 CAPLUS <<LOGINID::20110428>>
DN 117:105380
OREF 117:18205a,18208a
TI Mitotic recombination of ***yeast*** artificial chromosomes
AU Ragoussis, Jiannis; Trowsdale, John; Markie, David
CS Hum. Immunogenet., ICRF Lab., London, WC2A 3PX, UK

SO Nucleic Acids Research (1992), 20(12), 3135-8 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Large regions of human DNA can be cloned and mapped in ***yeast*** artificial chromosomes (YACs). Overlapping YAC clones can be used in order to reconstruct genomic segments in vivo by meiotic recombination. This is of importance for reconstruction of a long gene or a gene complex. In this work advantage was taken of ***yeast*** protoplast fusion to generate isosexual diploids followed by mitotic crossing-over, and showing that it can be an alternative simple strategy for recombining YACs. Integrative transformation of one of the parent strains with the construct pRAN4 (contg. the ADE2 ***gene***) is used to ***disrupt*** the URA3 ***gene*** contained within the pYAC4 vector arm, providing the ***markers*** required for forcing fusion and detecting recombination. All steps can be carried out within the commonly used AB1380 host strain without the requirement for micromanipulation. The method was applied to YAC clones from the human MHC and resulted in the reconstruction of a 650 kb long single clone contg. 18 known genes from the MHC class II region.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L11 ANSWER 100 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1992:211009 CAPLUS <<LOGINID::20110428>>
DN 116:211009
OREF 116:35655a,35658a
TI Specificity of unsaturated fatty acid-regulated expression of the ***Saccharomyces*** ***cerevisiae*** OLE1 gene
AU McDonough, Virginia M.; Stukey, Joseph E.; Martin, Charles E.
CS Nelson Biol. Lab., Rutgers Univ., Piscataway, NJ, 08855-1059, USA
SO Journal of Biological Chemistry (1992), 267(9), 5931-6 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The ***Saccharomyces*** ***cerevisiae*** OLE1 gene encodes the .DELTA.-9 fatty acid desaturase, an enzyme which forms the monounsatd. palmitoleic (16:1) and oleic (18:1) fatty acids from palmitoyl (16:0) or stearoyl (18:0) CoA. Previous studies demonstrated that OLE1 mRNA levels and desaturase enzyme activity are repressed when either 16:1 .DELTA.-9 and 18:1 .DELTA.-9 are added to the growth medium (1). The polyunsaturate, linoleic acid (18:2, .DELTA.-9,12), which is not a product of the enzyme, is also a strong repressor. The specificity of the OLE1 transcriptional regulatory sensor was examd. by testing the response of OLE1 promoter-lacZ fusion reporter genes to fatty acids that differ in chain length, degree of unsatn. and double bond positions. Monounsatd. and polyunsatd. fatty acids that contain a .DELTA.-9 double bond are strong repressors of reporter gene activity and native OLE1 mRNA levels. Monounsatd. fatty acids contg. double bonds in the .DELTA.-10, .DELTA.-11, or .DELTA.-5 positions showed no repression of ***reporter*** enzyme levels although they were rapidly incorporated into membrane lipids and some supported growth of an OLE1 ***gene*** ***disrupted*** strain. Although 17:1 .DELTA.-10 does not repress OLE1 transcription, lipid anal. showed that it replaces almost all of the endogenous 16:1 .DELTA.-9 and 18:1 .DELTA.-9 in cellular lipids and OLE1 mRNA levels are strongly repressed. This suggests that addnl. systems regulate desaturase activity by post-transcriptional mechanisms that differ from the transcriptional sensor in their responses to specific fatty acids.
OSC.G 76 THERE ARE 76 CAPLUS RECORDS THAT CITE THIS RECORD (76 CITINGS)

L11 ANSWER 101 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1992:35260 CAPLUS <<LOGINID::20110428>>
DN 116:35260
OREF 116:5897a,5900a
TI Repeated use of GAL1 for gene disruption in Candida albicans
AU Gorman, Jessica A.; Chan, Winnie; Gorman, John W.
CS Dep. Gene Expression Sci., Smith Kline Beecham Pharm., King of Prussia, PA, 19406, USA
SO Genetics (1991), 129(1), 19-24 CODEN: GENTAE; ISSN: 0016-6731
DT Journal
LA English
AB A technique which has the potential to allow repeated use of the same selectable ***marker*** to create ***gene*** ***disruptions*** in C. albicans has been developed. In this approach, originally described for ***Saccharomyces*** ***cerevisiae*** , the selectable marker is flanked by direct repeats. Mitotic recombination between these repeats leads to elimination of the selectable marker. A module in which the GAL1 gene is flanked by direct repeats of the bacterial CAT gene was constructed and used to disrupt one copy of the URA3 gene in a gal1 mutant. Gal- revertants were selected by plating on 2-deoxy-D-galactose (2DOG). The frequency 2DOG-resistant colonies recovered was 20 times higher than that obtained with a similar construct not flanked by direct repeats. Of these, 20% had lost the GAL1 gene by recombination between the direct repeats. The GAL1 gene was used again to disrupt the remaining wild-type copy of the URA3 gene of one of these gal1 isolates, resulting in a stable ura3 mutant. This technique should be generally appreciable to derive homozygous gene disruptions in this diploid organism.
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

L11 ANSWER 102 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1991:649615 CAPLUS <<LOGINID::20110428>>
DN 115:249615
OREF 115:42297a,42300a
TI Method for increasing the .omega.-hydroxylase activity of Candida tropicalis in the manufacture of .alpha.,.omega.-dicarboxylic acids
IN Picataggio, Stephen; Rohrer, Tracy; Eirich, L. Dudley
PA Henkel Research Corp., USA
SO PCT Int. Appl., 52 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 9114781 A1 19911003 WO 1991-US1864 19910315 W: CA, JP RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE US 5620878 A 19970415 US 1995-407429 19950317 US 5648247 A 19970715 US 1995-425124 19950419
PRAI US 1990-495502 A 19900319 US 1992-975154 B3 19921112
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB Recombinant C. tropicalis with increased .omega.-hydroxylase activity are prepd. These recombinant ***yeast*** produce .alpha.,.omega.-dicarboxylic acids at greater rates than the wild-type. Integrating vectors contg. the ***yeast*** URA3 gene and the cytochrome P450 monooxygenase or the NADPH-cytochrome reductase gene were prepd. C. tropicalis in which all four POX4 and POX5 ***genes*** are ***disrupted*** by a URA3 selectable ***marker*** were transformed with these plasmids. Strains contg. multiple monooxygense and reductase genes were isolated. Prodn. rates of .alpha.,.omega.-dicarboxylic acids with these chains were 25-30% higher than those of the wild-type parent.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 103 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1991:529049 CAPLUS <<LOGINID::20110428>>
DN 115:129049
OREF 115:21981a,21984a
TI The YDp plasmids: a uniform set of vectors bearing versatile gene disruption cassettes for ***Saccharomyces*** ***cerevisiae***
AU Berben, Gilbert; Dumont, Jacques; Gilliquet, Veronique; Bolle, Paul Andre; Hilger, Francois
CS Unite Microbiol., Fac. Sci. Agron. Gembloux, Gembloux, B-5030, Belg.
SO Yeast (1991), 7(5), 475-7 CODEN: YESTE3; ISSN: 0749-503X
DT Journal
LA English
AB The YDp plasmids (***Yeast*** ***Disruption*** plasmids) are pUC9 vectors bearing a set of ***yeast*** ***gene*** ***disruption*** cassettes, all uniform in structure and differing only in the selectable ***marker*** used (HIS3, LEU2, LYS2, TRP1, or URA3). The markers, surrounded by translational termination codons, are embedded in the slightly modified sequence of the pUC9 multiple cloning sites.
OSC.G 218 THERE ARE 218 CAPLUS RECORDS THAT CITE THIS RECORD (218 CITINGS)

L11 ANSWER 104 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1991:179667 CAPLUS <<LOGINID::20110428>>
DN 114:179667
OREF 114:30187a,30190a
TI Stable integration and expression in mouse cells of ***yeast*** artificial chromosomes harboring human genes
AU Eliceiri, Brian; Labella, Tullio; Hagino, Yoshi; Srivastava, Anand; Schlessinger, David; Pilia, Giuseppe; Palmieri, Giuseppe; D'Urso, Michele
CS Sch. Med., Washington Univ., St. Louis, MO, 63110, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1991), 88(6), 2179-83 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The authors developed a way to fit ***yeast*** artificial chromosomes (YACs) with markers that permit the selection of stably transformed mammalian cells, and detd. the fate and expression of such YACs contg. the genes for human rRNA (rDNA) or glucose-6-phosphate dehydrogenase (G6PD). The YACs in the ***yeast*** cell are retrofitted with selectable markers by homologous recombination with the URA3 gene of one vector arm. The DNA fragment introduced contains a LYS2 ***marker*** selective in ***yeast*** and a thymidine kinase (TK) ***marker*** selective in TK-deficient cells, bracketed by portions of the URA3 sequence that ***disrupt*** the endogenous ***gene*** during the recombination event. Analyses of transformed L-M TK- mouse cells showed that YACs contg. rDNA or G6PD were incorporated in essentially intact form into the mammalian cell DNA. For G6PD, a single copy of the transfected YAC was found in each of 2 transformants analyzed and was fully expressed, producing the expected human isoenzyme as well as the heterodimer composed of the human gene product and the endogenous mouse gene product.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L11 ANSWER 105 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1991:115901 CAPLUS <<LOGINID::20110428>>
DN 114:115901
OREF 114:19577a,19580a
TI Single-step selection for Ty1 element retrotransposition
AU Curcio, M. Joan; Garfinkel, David J.
CS Frederick Cancer Res. Dev. Cent., Natl. Cancer Inst., Frederick, MD, 21702-1201, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1991), 88(3), 936-40 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The ***yeast*** retrotransposon Ty1 has been tagged with a reporter gene that allows selection of RNA-mediated transposition events and is applicable to the study of retroelements in other organisms. The ***reporter*** ***gene*** is a ***yeast*** HIS3 ***gene*** ***interrupted*** by an artificial intron (AI) in the antisense orientation. The HIS3AI sequences were inserted into a Ty1 element such that the intron is on the sense strand of the Ty1 element; therefore, splicing and retrotransposition of marked Ty1 transcripts can give rise to His+ cells. Fusion of the Ty1-H3mHIS3AI element to the inducible GAL1 promoter resulted in a high frequency of histidine prototrophs upon galactose induction. Moreover, spontaneous His+ revertants derived from strains contg. genomic TymHIS3AI elements are a result of retrotransposition. By using this assay, the Ty1 transposition rate was estd. to be between 3 .times. 10-7 and 1 .times. 10-5 transpositions per Ty1 element per generation. Variations in the transposition rate of individual Ty1 elements are correlated with their relative abundance of their transcripts.
OSC.G 121 THERE ARE 121 CAPLUS RECORDS THAT CITE THIS RECORD (122 CITINGS)

L11 ANSWER 106 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1990:472268 CAPLUS <<LOGINID::20110428>>
DN 113:72268
OREF 113:12097a,12100a
TI ERS1 a seven transmembrane domain protein from ***Saccharomyces*** ***cerevisiae***
AU Hardwick, Kevin G.; Pelham, Hugh R. B.
CS Lab. Mol. Biol., MRC, Cambridge, CB2 2QH, UK
SO Nucleic Acids Research (1990), 18(8), 2177 CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English

AB The cloning and characterization of the ERD1 (ER Retention Defective) gene product from S. ***cerevisiae*** was recently reported. It is required for the retention of luminal endoplasmic reticulum proteins and for full glycoprotein processing in the Golgi app. Here, the sequence of another ***yeast*** membrane protein ERS1 (ERD Suppressor) is reported. The gene was isolated from a genomic library in YEp13 when attempting to clone the ERD1 gene by complementation. It was found, upon subcloning and re-transformation, that ERS1 significantly reduced the erd phenotype (the secretion of endogenous ER proteins and an invertase-HDEL ***marker*** construct used in the initial isolation of erd mutants of multiple erd1 alleles and a strain carrying a ***disrupted*** erd1 ***gene*** . Sequence and hydropathy anal. predict a 30 kD protein with 7 putative transmembrane domains. A gene disruption of ERS1 has been performed; the resulting strain is viable and does not have an erd phenotype.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L11 ANSWER 107 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1990:113244 CAPLUS <<LOGINID::20110428>>
DN 112:113244
OREF 112:19059a,19062a
TI Isolation of metabolic genes and demonstration of gene disruption in the phytopathogenic fungus Ustilago maydis
AU Kronstad, J. W.; Wang, J.; Covert, S. F.; Holden, D. W.; McKnight, G. L.; Leong, S. A.
CS Plant Dis. Resist. Unit, Agric. Res. Serv., Madison, WI, 53706, USA
SO Gene (1989), 79(1), 97-106 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB A cDNA library was constructed in the ***yeast*** expression vector pYcDE8 using mRNA from the phytopathogenic fungus U. maydis and cDNAs capable of complementing mutations in 3 ***yeast*** genes, URA3, LEU2 and TPI1, were identified. Nucleotide sequence anal. indicated that the cDNA clone, which complemented the ***yeast*** ura3 mutation, carries the pyr6 gene encoding orotidine-5'-phosphate dcecarboxylase. The genomic copy of the pyr6 gene was isolated by hybridization with the cDNA and used to complement a pyr- mutant of U. maydis. One-step ***gene*** ***disruption*** was demonstrated by transforming U. maydis with a copy of the pyr6 ***gene*** ***interrupted*** in the coding region by a selectable ***marker*** for resistance to hygromycin B.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)

L11 ANSWER 108 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1990:3498 CAPLUS <<LOGINID::20110428>>
DN 112:3498
OREF 112:707a,710a
TI The role of subunit 4, a nuclear-encoded protein of the F0 sector of ***yeast*** mitochondrial ATP synthase, in the assembly of the whole complex
AU Paul, Marie Francoise; Velours, Jean; Arselin de Chateaubodeau, Genevieve; Aigle, Michel; Guerin, Bernard
CS Inst. Biochim. Cell. Neurochim., Univ. Bordeaux, Bordeaux, F-33077, Fr.
SO European Journal of Biochemistry (1989), 185(1), 163-71 CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
AB ***Yeast*** nuclear ***gene*** ATP4, encoding ATP synthase subunit 4, was ***disrupted*** by insertion into the middle of it the selective ***marker*** URA3. The transformation of the ***Saccharomyces*** ***cerevisiae*** strain D273-10B/A/U produced a mutant unable to grow on glycerol medium. The ATP4 gene is unique since subunit 4 was not present in mutant mitochondria; the hypothetical truncated subunit 4 was never detected. ATPase was rendered oligomycin-insensitive and the F1 sector of this mutant appeared loosely bound to the membrane. Anal. of mitochondrially translated hydrophobic subunits of F0 revealed that subunits 8 and 9 were present, unlike subunit 6. This indicated a structural relation between subunits 4 and 6 during biogenesis of F0. It therefore appears that subunit 4 (also called subunit b in bovine heart and Escherichia coli ATP synthases) plays at least a structural role in the assembly of the whole complex. Disruption of the ATP4 gene also had a dramatic effect on the assembly of other mitochondrial complexes. Thus, the cytochrome oxidase activity of the mutant strain was .apprx.5-fold lower than that of the wild type. In addn., a high percentage of spontaneous rho- mutants was detected.
OSC.G 58 THERE ARE 58 CAPLUS RECORDS THAT CITE THIS RECORD (58 CITINGS)

L11 ANSWER 109 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1989:170087 CAPLUS <<LOGINID::20110428>>
DN 110:170087
OREF 110:28129a,28132a
TI L-Canavanine resistance as a positive selectable ***marker*** in diploid ***yeast*** transformation through integral ***disruption*** of the CAN1 ***gene***
AU Suizu, Tetsuyoshi; Iimura, Yuzuru; Gomi, Katsuya; Takahashi, Kojiro; Hara, Shodo; Yoshizawa, Kiyoshi
CS Natl. Res. Inst. Brew., Tokyo, 114, Japan
SO Agricultural and Biological Chemistry (1989), 53(2), 431-6 CODEN: ABCHA6; ISSN: 0002-1369
DT Journal
LA English
AB A novel transformation system was developed for yeasts carrying no selectable markers. By using a plasmid, pYHH-1, contg. an internal region of the CAN1 gene, a wild-type ***yeast*** strain was endowed with L-canavanine resistance (can1) through integral disruption of the resident CAN1 gene. Diploid strains as well as haploids can be transformed, indicating that L-canavanine resistance can be used as a pos. selectable marker for the transformation of industrial yeasts.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L11 ANSWER 110 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1987:434290 CAPLUS <<LOGINID::20110428>>
DN 107:34290
OREF 107:5647a,5650a
TI Cloning and heterologous expression of glycosidase genes from ***Saccharomyces*** ***cerevisiae***
AU Kuranda, Michael J.; Robbins, Phillips W.
CS Cent. Cancer Res., Massachusetts Inst. Technol., Cambridge, MA, 02139, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1987), 84(9), 2585-9 CODEN: PNASA6; ISSN: 0027-8424
DT Journal

LA English
AB Genomic clones were isolated that code for three glycosidases proposed to be involved in the catabolism of cell wall components in S. ***cerevisiae*** . .alpha.-Mannosidase (AMS1), exoglucanase (BGL1), and endochitinase (CTS1) genes were isolated with the aid of filter assays based on the hydrolysis of 4-methylumbelliferyl glycosides, which permitted the in situ monitoring of these glycosidase activities in ***yeast*** colonies. Uracil prototrophs resulting from transformation with a multicopy YEp24 ***yeast*** genomic library were screened, leading to the identification of transformants possessing high levels of glycosidase activity. Restriction maps of plasmids from multiple isolates were used to localize glycosidase-overprodn. genes, which were subcloned into a Schizosaccharomyces pombe/S. ***cerevisiae*** shuttle vector. Transformation of S. pombe with BGL1 and CTS1 subclones resulted in the appearance of these activities in this organism, and an AMS1 plasmid caused a 2-fold increase in endogenous .alpha.-mannosidase levels. Insertion of the ***marker*** ***gene*** LEU2 into putative AMS1 sequences ***disrupted*** plasmid-encoded .alpha.-mannosidase overprodn. S. ***cerevisiae*** Strains that incorporated a restriction fragment contg. ams1::LEU2 into their chromosomal DNA by homologous recombination expressed no detectable .alpha.-mannosidase activity in either the haploid or homozygous recessive diploid states, whereas heterozygous and wild-type cells exhibited levels proportional to AMS1 gene dosage. No readily apparent phenotype was assocd. with the .alpha.-mannosidase deficiency; however, labeling expts. utilizing [2-3H]mannose suggest that .alpha.-mannosidase may function in mannan turnover.
OSC.G 41 THERE ARE 41 CAPLUS RECORDS THAT CITE THIS RECORD (41 CITINGS)

L11 ANSWER 111 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1986:566120 CAPLUS <<LOGINID::20110428>>
DN 105:166120
OREF 105:26681a,26684a
TI Genetic analyses of snRNAs and RNA processing in ***yeast***
AU Guthrie, Christine; Riedel, Nora; Parker, Roy; Swerdlow, Harold; Patterson, Bruce
CS Dep. Biochem. Biophys., Univ. California, San Francisco, CA, 94143, USA
SO UCLA Symposia on Molecular and Cellular Biology, New Series (1986), 33(Yeast Cell Biol.), 301-21 CODEN: USMBD6; ISSN: 0735-9543
DT Journal
LA English
AB The unique genetic capabilities of ***Saccharomyces*** ***cerevisiae*** were employed to det. the functions of small nuclear RNAs (snRNAs). SnRNAs are thought to mediate a spectrum of RNA processing events in eukaryotic cells. The 1st step in the genetic approach used was to clone the ***genes*** , ***disrupt*** them by insertion of a ***yeast*** selectable ***marker*** , and replace each resident chromosomal ***gene*** with its ***disrupted*** counterpart. At least 2 SNR genes are completely dispensable; moreover, the double mutant is not even growth-impaired. In a 3rd case, the snRNA gene product is essential for viability. In a complementary approach, the involvement of snRNAs in mRNA splicing was tested directly.

L11 ANSWER 112 OF 112 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1982:486267 CAPLUS <<LOGINID::20110428>>
DN 97:86267
OREF 97:14273a,14276a
TI Lethal disruption of the ***yeast*** actin gene by integrative DNA transformation
AU Shortle, David; Haber, James E.; Botstein, David
CS Dep. Biol., Massachusetts Inst. Technol., Cambridge, MA, 02139, USA
SO Science (Washington, DC, United States) (1982), 217(4557), 371-3 CODEN: SCIEAS; ISSN: 0036-8075
DT Journal
LA English
AB A mutant allele of the chromosomal locus corresponding to the cloned actin gene of ***Saccharomyces*** ***cerevisiae*** was constructed by DNA transformation with a hybrid plasmid which integrates into, and thereby disrupts, the protein-encoding sequences of the gene. In a diploid strain of ***yeast*** , ***disruption*** of the actin ***gene*** on 1 chromosome results in a mutation that segregates as a recessive lethal tightly linked to a selectable genetic ***marker*** on the integrated plasmid. The actin gene, therefore, must encode an essential function for ***yeast*** cell growth.
OSC.G 49 THERE ARE 49 CAPLUS RECORDS THAT CITE THIS RECORD (49 CITINGS)

=> d his
(FILE 'HOME' ENTERED AT 16:01:54 ON 28 APR 2011)
FILE 'CAPLUS' ENTERED AT 16:02:19 ON 28 APR 2011
L1 670 S ((GENE#(10A)(DISRUPT? OR INTERRUPT?))(30A)(MARKER? OR REPORTE
L2 291491 S (YEAST OR SACCHAROMYCES OR CEREVISIAE)/BI,AB
L3 178 S L1 AND L2
L4 172 S L3 NOT 2011/PY
L5 167 S L4 NOT 2010/PY
L6 159 S L5 NOT 2009/PY
L7 150 S L6 NOT 2008/PY
L8 140 S L7 NOT 2007/PY
L9 131 S L8 NOT 2006/PY
L10 116 S L9 NOT 2005/PY
L11 112 S L10 NOT 2004/PY

=> log y
COST IN U.S. DOLLARS SINCE FILE
TOTAL ENTRY SESSION
FULL ESTIMATED COST 419.20 419.43

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE TOTAL ENTRY SESSION
CA SUBSCRIBER PRICE -97.44 -97.44

STN INTERNATIONAL LOGOFF AT 16:07:08 ON 28 APR 2011